

NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

RELATED APPLICATIONS

This application claims priority to U.S.S.N. 60/167,383, filed November 24, 1999, which is incorporated herein by reference in its entirety.

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BACKGROUND OF THE INVENTION

Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. The approach is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in identity and paternity analysis, and in genetic mapping studies.

One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPs can create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is an alteration in the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences typically include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be referred to as a “cSNP” to denote that the nucleotide sequence containing the SNP

originates as a cDNA.

SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at which one allele bears a gap with respect to a single nucleotide in another allele.

Some SNPs occur within, or near genes. One such class includes SNPs falling within regions of genes encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, *e.g.*, genetic disease. Examples of genes in which a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the genome. The frequency and uniformity of SNPs means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest.

SUMMARY OF THE INVENTION

The invention is based in part on the discovery of novel single nucleotide polymorphisms (SNPs) in regions of human DNA.

Accordingly, in one aspect, the invention provides an isolated polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 1468) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it

includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS: 1-1468), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

5 The polynucleotide can be, *e.g.*, DNA or RNA, and can be between about 10 and about 100 nucleotides, *e.g.*, 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

In some embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, *e.g.*, the polymorphic site includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

10 In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of the polymorphic sequence, *e.g.*, the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

15 In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to an ATPase associated protein, a cadherin, or any of the other proteins identified in Table 1, column 10.

20 In another aspect, the invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the complementary nucleotide

sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

5 In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, e.g., (a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence; (b) a nucleotide sequence that is a fragment of 10 any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), wherein the polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

15 The oligonucleotide can be, e.g., between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

20 The invention also provides a method of detecting a polymorphic site in a nucleic acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the 25 nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, 5 column 5 for the polymorphic sequence.

The oligonucleotide can be, e.g., between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

In some embodiments, the polymorphic sequence identified by the 10 oligonucleotide is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated polypeptide related to an ATPase associated protein, cadherin, or any of the other protein families identified in Table 1, column 10.

In another aspect, the method includes determining if a sequence polymorphism is 15 present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the 20 complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In a further aspect, the invention provides a method of determining the relatedness 25 of a first and second nucleic acid. The method includes providing a first nucleic acid and a second nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1,

column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids to the nucleic acid indicates the first and second subjects are related.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, e.g., between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from the child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences SEQ ID NOS:1-1468, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the

complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, *e.g.*, related to one of the protein families disclosed herein. For example, polypeptide can be related to an ATPase associated protein,
5 cadherin, or any of the other proteins provided in Table 1, column 10.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

10 In some embodiments, the polypeptide encoded by the polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

15 The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-1468, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

20 In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

25 Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The

method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen complexes. The antibody-antigen complexes are then detected. The presence of the complexes indicates the presence of the polypeptide.

5 The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, *e.g.*, a human, non-human primate, cat, dog, rat, mouse, cow, pig, goat, or rabbit. The method includes providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic 10 sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively different polypeptides 15 can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene. Finally, 20 aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

The therapeutic agent can include, *e.g.*, second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence 25 comprises a polymorphic sequence which includes nucleotide listed in Table 1, column 5 for the polymorphic sequence.

Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is

complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an
5 oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for the polymorphic sequence.

In another aspect, the invention provides an oligonucleotide array comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468); a nucleotide sequence that is a fragment of any of the nucleotide sequences, provided that the
10 fragment includes a polymorphic site in the polymorphic sequence; a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468); or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.
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In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described nucleic acids. The kit can include, *e.g.*, a polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 1468) and which includes a polymorphic sequence, or a
20 fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS:1-1468), or a
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fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence. The invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, e.g., a nucleotide sequence comprising 5 one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary 10 nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the 15 fragment includes a polymorphic site in the polymorphic sequence.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable 20 methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

25 Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides human SNPs in sequences which are transcribed, *i.e.*, are cSNPs. As is explained in more detail below, many SNPs have been identified in genes related to polypeptides of known function. For some applications, SNPs associated with various polypeptides can be used together. For example, SNPs can be group according to whether they are derived from a nucleic acid encoding a polypeptide related to a particular protein family or involved in a particular function. Thus, SNPs related to ATPase associated protein may be collected for some applications, as may SNPs associated with cadherin, or ephrin (EPH), or any of the other proteins recited in Table 1, column 10. Similarly, SNPs can be grouped according to the functions played by their gene products. Such functions include, *e.g.*, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism.

The SNPs are shown in Table 1 and the Sequence Listing. Both provide a summary of the polymorphic sequences disclosed herein. In the Table, a “SNP” is a polymorphic site embedded in a polymorphic sequence. The polymorphic site is occupied by a single nucleotide, which is the position of nucleotide variation between the wild type and polymorphic allelic sequences. The site is usually preceded by and followed by relatively highly conserved sequences of the allele (*e.g.*, sequences that vary in less than 1/100 or 1/1000 members of the populations). Thus, a polymorphic sequence can include one or more of the following sequences: (1) a sequence having the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence; or (2) a sequence having a nucleotide other than the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence. An example of the latter sequence is a polymorphic sequence having the nucleotide denoted in Table 1, column 6 at the polymorphic site in the polymorphic sequence.

Nucleotide sequences for a referenced-polymorphic pair are presented in Table 1. Each cSNP entry provides information concerning the wild type nucleotide sequence as well as the corresponding sequence that includes the SNP at the polymorphic site. Since

the wild type sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele; its SEQ ID NO: is also cross referenced in the Table 1. A reference to the SEQ ID NO: giving the translated amino acid sequence is also given if appropriate. The Table includes thirteen columns 5 that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

“SEQ ID” provides the cross-reference to the nucleotide SEQ ID NO:, and, as explained below, an amino acid SEQ ID NO: as well, in the Sequence Listing of the application. Conversely, each sequence entry in the Sequence Listing also includes a 10 cross-reference to the CuraGen sequence ID, under the label “CuraGen Sequence ID”. The first SEQ ID NO: given in the first column of each row of the Table is the SEQ ID NO: identifying the nucleic acid sequence for the polymorphism. If a polymorphism carries an entry for the amino acid portion of the row, a second SEQ ID NO: appears in parentheses in the column “Amino acid after” (see below). This second SEQ ID NO: 15 refers to an amino acid sequence giving the polymorphic amino acid sequence that is the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one SEQ ID NO: is provided.

“CuraGen sequence ID” provides CuraGen Corporation’s accession number.

“Base pos. of SNP” gives the numerical position of the nucleotide in the 20 reference, or wild-type, gene at which the cSNP is found. This enumeration of bases is that found in the public database from which the reference gene is taken (see column headed “Name of protein identified following a BLASTX analysis of the CuraGen sequence”) as of the filing date of the instant application.

“Polymorphic sequence” provides a 51-base sequence with the polymorphic site 25 at the 26th base in the sequence, as well as 25 bases from the reference sequence on the 5' side and the 3' side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a “slash (/”); and third, the polymorphic nucleotide. In certain cases the polymorphism is an

insertion or a deletion. In that case, the position which is "unfilled" (i.e., the reference or the polymorphic position) is indicated by the word "gap".

"Base before" provides the nucleotide present in the reference, or wild-type, gene at the position at which the polymorphism is found.

5 "Base after" provides the altered nucleotide at the position of the polymorphism.

"Amino acid before" provides the amino acid in the reference protein, if the polymorphism occurs in a coding region.

"Amino acid after" provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in 10 parentheses if the polymorphism occurs in a coding region.

"Type of change" provides information on the nature of the polymorphism.

"SILENT-NONCODING" is used if the polymorphism occurs in a noncoding region of a nucleic acid.

15 "SILENT-CODING" is used if the polymorphism occurs in a coding region of a nucleic acid of a nucleic acid and results in no change of amino acid in the translated polymorphic protein.

"CONSERVATIVE" is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are:

20 Aliphatic: Gly, Ala, Val, Leu, Ile;

Aromatic: Phe, Tyr, Trp;

Sulfur-containing: Cys, Met;

Aliphatic OH: Ser, Thr;

Basic: Lys, Arg, His;

Acidic: Asp, Glu, Asn, Gln;

Pro falls in none of the other classes; and

End defines a termination codon.

5 “NONCONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

“FRAMESHIFT” relates to an insertion or a deletion. If the frameshift occurs in a coding region, the Table provides the translation of the frameshifted codons 3' to the polymorphic site.

10 “Protein classification of CuraGen gene” provides a generic class into which the protein is classified. During the course of the work leading to the filing of this application, several classes of proteins were identified. Some are described further below.

15 “Name of protein identified following a BLASTX analysis of the CuraGen sequence” provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely.

20 “Similarity (pvalue) following a BLASTX analysis” provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of pvalue > 1 x 10⁻⁵⁰ (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel. A pvalue < 1 x 10⁻⁵⁰ defines proteins considered to be already known.

“Map location” provides any information available at the time of filing related to localization of a gene on a chromosome.

25 The polymorphisms are arranged in the Table in the following order.

SEQ ID NOs: 1-722 are SNPs that are silent.

SEQ ID NOs: 723-797 are SNPs that lead to conservative amino acid changes.

SEQ ID NOs: 798-989 are SNPs that lead to nonconservative amino acid changes.

5 SEQ ID NOs: 990-1095 are SNPs that involve a gap. With respect to the reference or wild-type sequence at the position of the polymorphism, the allelic cSNP introduces an additional nucleotide (an insertion) or deletes a nucleotide (a deletion). An SNP that involves a gap generates a frame shift.

10 SEQ ID NOs: 1096-1170 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 723-797. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

15 SEQ ID NOs: 1171-1362 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 798-989. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

20 SEQ ID NOs: 1363-1468 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to frameshift-induced amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 990-1095. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

IDENTIFICATION OF INDIVIDUALS CARRYING SNPs

5 Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of
10 polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by *e.g.*, PCR. See generally PCR Technology: Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

20 The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, i.e., a "polymorphic protein" containing an altered amino acid at the site of translation of the nucleotide
25 polymorphism. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The phrase "substantially purified" or "isolated" when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or preferably, essentially none, of other cellular components with which it is naturally associated. Thus, the phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as gel electrophoresis or high performance liquid chromatography. Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J & 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art. A "nucleic acid" is a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term "nucleic acids", as used herein, refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide

bases read from the 5' end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence.

10 “Nucleic acid probes” may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy *Lancet* ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. *Nucl. Acids Res.* 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. *Proc. Natl. Acad. SCI. USA*, 86:6230-6234 (1969)) or oligonucleotide arrays (Maskos and Southern *Nucl. Acids Res.* 21:2269-2270 (1993)), allele-specific PCR (Newton et al. *Nucl Acids Res* 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox *Genome Res* 5:474-482 (1995)), binding of MutS protein (Wagner et al. *Nucl Acids Res* 23:3944-3948 (1995)), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. *Proc. Natl. Acad. Sci. U.S.A.* 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. *Genomics* 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. *Science* 230:1242 (1985)), chemical (Cotton et al. *Proc. Natl. w Sci. U.S.A.*, 8Z4397-4401 (1988)) or enzymatic (Youil et al. *Proc. Natl. Acad. Sci. U.S.A.* 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvanen et al. *Genomics* 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. *&&I Acids* 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. *Science* 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany *Proc. Natl. Acad. Sci. U.S.A.* 88:189-193 (1991)), gap-LCR (Abravaya et al. *Nucl Acids Res* 23:675-682 (1995)), radioactive and/or fluorescent

DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., Nucl. Acids Res, 21:5332-5356 (1993); Thiede et al., Nucl. Acids Res. 24:983-984 (1996)).

“Specific hybridization” or “selective hybridization” refers to the binding, or duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). “Stringent conditions” are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point (Tm) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridization.

“Complementary” or “target” nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe’s length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or Current Protocols in Molecular Biology, F. Ausubel et al., ed., Greene Publishing and Wiley-Interscience, New York (1987).

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A "polymorphic" marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include
5 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative,
10 variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.

15 As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of a complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen
20 bond formation. Oligonucleotides probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization.
25

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate
30 conditions (e.g., in the presence of four different nucleoside triphosphates and a

polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to 5 form sufficiently stable hybrid complexes with the template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA 10 sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett 22:1859-1 862 (1981) and the triester method provided by Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., Nucleic Acids Res. 12:61596168 (1984).
15 20 Purification of oligonucleotides may be carried out by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand using a DNA 25 polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The sequence of the synthetic oligonucleotide or of any nucleic acid fragment 30 can be obtained using either the dideoxy chain termination method or the Maxam-

Gilbert method (see Sambrook et al. Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al." ; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, 5 (Acad. Press, New York). Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule 10 comprising the SNP-containing nucleotide sequences of the invention, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid 15 molecules are provided that comprise a sequence complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire SNP coding strand, or to only a portion thereof.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons 20 which are translated into amino acid. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred 25 to as 5' and 3' untranslated regions).

Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to the entire coding region of an mRNA, but more preferably as

embodied herein, it is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more 5 preferably between about 15 and 30 in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the 10 molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, 15 hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 20 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 25 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a

complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 852444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described generally in Sambrook et al., The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assay of genomic DNA, virtually any biological convenient tissue sample can be used. Suitable samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair can be used. Genomic DNA is typically amplified before

analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the 5 amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNase.

DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE

10 The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, 15 Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe 20 hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7, 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

25 Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in published PCT application WO 95/11995. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be 5 complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are 10 expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on a target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17 2427-2448 (1989). 15 This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method 20 works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be 25 analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated and 5 heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

10 The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, 15 familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

20 Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, system, diseases of the nervous and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the 25 bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach, leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are 5 within a 50,000 bp region in the human genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an 10 unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

15 The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not 20 match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical 25 analysis to determine the probability that a match of suspect and crime scene sample would occur by chance.

p(ID) is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with 30 frequencies x and y, the probability of each genotype in a diploid organism are (see WO

95/12607):

$$\text{Homozygote: } p(AA) = x^2$$

$$\text{Homozygote: } p(BB) = y^2 = (1-x)^2$$

$$\text{Single Heterozygote: } p(AB) = p(BA) = xy = x(1-x)$$

5 Both Heterozygotes: $p(AB+ BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

10 These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

15 In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($\text{cum } p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$\text{cum } p(ID) = p(ID_1)p(ID_2)p(ID_3)\dots p(ID_n)$$

20 The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

5 The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in
10 the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation
15 can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc})=xy(1-xy)$$

20 where x and y are the population frequencies of alleles A and B of a diallelic polymorphic site. (At a triallelic site $p(\text{exc})=xy(1-xy)+yz(1-yz)+xz(1-xz)+3xyz(1-xyz))$, where x, y and z are the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

$$p(\text{non-exc})=1-p(\text{exc})$$

25 The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc})=p(\text{non-exc}1)p(\text{non-exc}2)p(\text{non-exc}3)\dots p(\text{non-exc}n)$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded) is:

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic

treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic marker sets.

To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a

5 polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods and statistically significant correlations between

10 polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

15 Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious

20 disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be

25 motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this

treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value

is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction RF , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (RF), ranging from $RF=0.0$ (coincident loci) to $RF=0.50$ (unlinked). Thus, the likelihood at a given value of RF is: probability of data if loci linked at RF to probability of data if loci unlinked. The computed likelihood is usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of RF (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of RF at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of RF) than the possibility that the two loci are unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved

by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned 5 variant gene is inactivated by insertion of a positive selection marker. See Capecchi, Science 244, 1288-1292. The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

10 The invention further provides methods for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug targets have been correlated with individual differences based on distinction in 15 the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmacogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

20 In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the cause of a pathological condition, method of treating such a condition includes administering to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

25 A subject suspected of suffering from a pathology ascribable to a polymorphic protein that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by

administering a normal or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid may be administered include incorporating the wild-type gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For

example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. Gene 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, Science 196:180-182 (1977). Colony hybridization is carried out as generally described in M. Grunstein et al. Proc. Natl. Acad. Sci. USA. 72:3961-3965 (1975). DNA of interest is identified in either cDNA or

genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders 5 of the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be 10 used in a variety of protocols to isolate cDNAs encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one 15 can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in 20 prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either 25 prokaryotes or eukaryotes. Typical expression vectors contain initiation sequences, transcription and translation terminators, and promoters useful for regulation of the expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for

translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and 5 eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a 10 strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacterial. 158:1018-1024 (1984) and the leftward promoter of phage lambda as described by A, I. and Hagen, D., Ann. 15 Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during 20 purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the 25 expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the

invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the 5 protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., Gene 8:17-24 (1979); Broach, et al., Gene 8:121-133 (1979)).

10 Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glusulase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, Nature (London) 275:104-109 (1978); and 15 Hinnen, A., et al., Proc. Natl. Acad. Sci. USA, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., J. Bact, 153:163-168 (1983)) cells and applying standard protein isolation techniques to the lysates.:.

20 The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian 25 cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can 30 include expression control sequences, such as an origin of replication, a promoter (e.g.,

the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen et al. Immunol. Rev., 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.

- 5 Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and Drosophila cell lines such as a Schneider cell line (See Schneider J. Embryol. Exp. Morphol., 27:353-365 (1987). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known 10 mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV4O (Sprague, J. et al., J. Virol. 45: 773-781 15 (1983)). Additionally, gene sequences to control replication in the host cell may be 20 Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known methods of introducing 25 DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or 30

as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the gene encoding the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated nucleotide sequences. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains,

Candida or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced 5 therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for 10 baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac© kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention 15 is "transformed." The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.

The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known 20 conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. 25 Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may be purified to substantial purity by standard

techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, Protein Purification: Principles and Practice, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl@ or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal, 5 monoclonal, chimeric, single chain, F_{ab} and F_{(ab')2} fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically immunoreactive with", an antibody when referring to a protein or peptide, 10 refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody 15 that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select 20 monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) Antibodies, a Laboratory Manual, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

Polyclonal and/or monoclonal antibodies that immunospecifically bind to 25 polymorphic gene products but not to the corresponding prototypical or "wild-type" gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, Antibodies, A Laboratory Manual, Cold Spring Harbor Press, New York (1988); Goding, Monoclonal antibodies, Principles 30 and Practice (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are

tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that binds the polymorphic protein using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the surface of the protein, *e.g.*, hydrophilic regions.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography, to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that originates from the clone of a singly hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polymorphic protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a polymorphic protein (see e.g., U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See e.g., U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab')2} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab')2} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by 5 recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; 10 Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988) *J Natl Cancer Inst* 80:1553-1559; Morrison(1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. 15 No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeven *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060.

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the 20 art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived 25 CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as

immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance.

10 Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

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EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that unique compositions and methods of use thereof in SNPs in known genes have been described. Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims which follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims.

Table 1

| 1 Seq ID | 2 CuraGen sequence ID | 3 Base pos. of SNP | 4 Polymorphic sequence | 5 Base before | 6 Base after | 7 Amino acid before | 8 Amino acid after | 9 Type of change | 10 Protein classification of CuraGen gene | 11 Name of protein identified following a BLASTX analysis of the CuraGen sequence | 12 Similarity (pValue) following a BLASTX analysis | 13 Map location |
|--------------|--------------------------|--|---------------------------|------------------|-----------------|------------------------|-----------------------|---------------------|--|--|---|--------------------|
| 1 cg43921971 | 1030 | GGGTTTGTATTG GCGCACCAAGA TC[T/C]CCAACA GCCAGTGTGTG TTTCCCAT | T | C | | | | SILENT-NONCODING | apoptosis | Human Gene Similar to SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa. | 6.10E-68 | |
| 3 cg43314087 | 475 | ATGGGGTTTTTT GTTTTTGTTTT GT/gap]TTTTT TTAAAGGCAAAG GGGTCT | T | gap | | | | SILENT-NONCODING | ATPase-associated | Human Gene SWISSPROT-ID:P14415 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) - HOMO SAPIENS (HUMAN), 290 aa. | 4.00E-160 | 17 (17p) |
| 4 cg43314087 | 484 | TTTGGGGTTTGT TTGGTTTTTTT T/gap]AAAGGCA AAGGGGTCTGA AGAGATG | T | gap | | | | SILENT-NONCODING | ATPase-associated | Human Gene SWISSPROT-ID:P14415 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) - HOMO SAPIENS (HUMAN), 290 aa. | 4.00E-160 | 17 (17p) |
| 5 cg43132502 | 200 | CATGAGGTGGC ACGAGGCCAGGA GTT[G/gap]GCGA TGCCACCTGGG GGTCACATTG | G | gap | | | | SILENT-NONCODING | ATPase-associated | Human Gene Similar to SPTREMBL-ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa. | 9.40E-58 | 11 |
| 6 cg43988460 | 4698 | ACATAATTGGTA CCAAAAAA A[A/gap]GAAAGG AAAGAAAAGGGG TGGCTGAA | A | gap | | | | SILENT-NONCODING | cadherin | Human Gene SWISSPROT-ID:P19022 NEURAL-CADHERIN PRECURSOR (N-CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa. | 0.00E+00 | 18 (18q11.2) |

| | | | | | | | | | | |
|----|-------------|------|--|---|-----|----------------------|----------------------|--|----------|------------------|
| 7 | cg43988460 | 4708 | TACCAAAAAAA AAAGGAAAGGA AA[G/A]AAGGG GTGCCCTGACA CTGGTGGC | G | A | SILENT- NONCODING | cadherin | Human Gene SWISSPROT- ID:P19022 NEURAL-CADHERIN PRECURSOR (N-CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa. | 0.00E+00 | 18 (18q11.2) |
| 8 | cg43982945 | 460 | GACACATGTCA GGCTGGGGCAG CAG[C/gap]CACT CTGATCAGCAC CAGGTTCCCGA | C | gap | SILENT- NONCODING | cathpsi | Human Gene Similar to SWISSPROT- ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa. | 2.00E-80 | 11 |
| 9 | cg43266931 | 96 | GGGGCCTAGCG GGGGTGCACGG CGG[G/gap]CG GTAGGCCGCCA GGATCTCGGCG | G | gap | SILENT- NONCODING | chloride_ channel | Human Gene Similar to SWISSPROT- ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa. Ipcis:SWISSPROT-ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa. | 3.10E-59 | 9 |
| 10 | cg43321451 | 1126 | GAAGGCCACACA CACACACAC ACA[C/gap]AGCA AAAGCTAAATCA TCACCGCG | C | gap | SILENT- NONCODING | collagen | Human Gene SWISSPROT- ID:Q99715 COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa. Ipcis:SPTREMBL-ID:Q99715 COLLAGEN TYPE XII ALPHA-1 PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa. | 0.00E+00 | 6 |
| 11 | cg439333757 | 3195 | TCATCTCCCTGC AACCTCGGCC CCT[C/ggg]TC AAGCGATTCTTG TGCCCTCA | T | C | SILENT- NONCODING | complement | Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa. | 0.00E+00 | 5 (5p13) |
| 12 | cg439333757 | 3212 | CCGCCCTCCCTGG GTTCAAGCGATT CTT[C/gtg]GCCT CAGGCCCTCCCAA GCAGCTGG | T | C | SILENT- NONCODING | complement | Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa. | 0.00E+00 | 5 (5p13) |

| | | | | | | | | | | |
|----|------------|------|---|----------|--|----------------------|----------------|---|-----------|----------|
| 13 | cg43933757 | 3346 | TCCAACCTCCTGA CCTCAGGGTAATC C[G/A]CCTGCCT TGGCTCCAA AGTGCTG | G A | | SILENT- NONCODING | complem ent | Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa. | 0.00E+00 | 5 (5p13) |
| 14 | cg42185571 | 2224 | CTTAGCTCTACG ATTAAATCCAT GTT/gapGCCAA GGGGAAAAACA TATTATA | T gap | | SILENT- NONCODING | complem ent | Human Gene SWISSPROT- ID:P02748 COMPLEMENT COMPONENT C9 PRECURSOR - HOMO SAPIENS (HUMAN), 559 aa. | 7.70E-308 | 5 (5p13) |
| 15 | cg42185571 | 2367 | TAATATAGATAG TGTTCAAGTAGCA G[A]gapATAGAA TGAAACATAAAACT ATTAGTT | A gap | | SILENT- NONCODING | complem ent | Human Gene SWISSPROT- ID:P02748 COMPLEMENT COMPONENT C9 PRECURSOR - HOMO SAPIENS (HUMAN), 559 aa. | 7.70E-308 | 5 (5p13) |
| 16 | cg43947909 | 265 | GAATTGTCCAGAC AGACTTGGCTC AG[C/T]GGAGG AGCTGATAGAC ATGGCTGT | C T | | SILENT- NONCODING | complem ent | Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q- R PROTEIN) (HYALURONAN- BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa. | 6.9E-129 | 17 |

| | | | | | | | | | | |
|----|------------|------|---|---|-----|----------------------|----------------|---|----------|---------------|
| 17 | cg43143315 | 2860 | GTGTGTGTCTC TC[C/G]GTAT GTGTGTGGG TTCTAATG | G | | SILENT- NONCODING | cyto450 | Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa. pcls:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa. | 1.9E-279 | 20 |
| 18 | cg43327428 | 1746 | AGCAGGGCTGGCA CTATGTGGTCTA AG[A/G]TTTCAGC CTGAAACTCATAG GACACTG | A | G | SILENT- NONCODING | cyto450 | Human Gene SWISSNEW-ID:P04798 CYTOCHROME P450 1A1 (EC 1.14.14.1) (CYPIA1) (P450-P1) (P450 FORM 6) (P450-C) - HOMO SAPIENS (HUMAN), 512 aa. pcls:SWISSPROT-ID:P04798 CYTOCHROME P450 1A1 (EC 1.14.14.1) (P450-P1) (P450 FORM 6) (P450-C) (TCDD-INDUCIBLE) - HOMO SAPIENS (HUMAN), 512 aa. | 2.5E-279 | 15 (15q22) |
| 19 | cg32296860 | 376 | CAGCACTTTGG GAGGCCGAGGC GGGT[C]GGATC ACCCGAGGTCA GGAGTTCGA | T | C | SILENT- NONCODING | cytochro me | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)- CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.6E-124 | |
| 20 | cg32296860 | 383 | TTGGGAGGGCCG AGGGGGTGGGA TCA[C/gap]CCGA GGTCAGGAGTT CGAGACCAGC | C | gap | SILENT- NONCODING | cytochro me | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)- CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.6E-124 | |

| | | | | | | | | | |
|----|------------|-----|---|---|-----|----------------------|-------------------|---|-----------|
| 21 | cg32296860 | 385 | GGGAGGGCGAG GGGGGTGGATC ACCI[C/gap]GAG GTCAGGGAGTTC GAGACCAGCCT | C | gap | SILENT- NONCODING | cytochro me | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)- CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.6E-124 |
| 22 | cg32296860 | 397 | CGGGTGGATCA CCCGAGGTCA GAG[T]TCGAG ACCAGCCTGGC CAACATGGT | T | A | SILENT- NONCODING | cytochro me | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)- CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.60E-124 |
| 23 | cg32296860 | 439 | CAACATGGTGA AACCCCTGTCTCT ACIT[C]AAAATA CAAAAATTAGCT GGGTGC | T | C | SILENT- NONCODING | cytochro me | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)- CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.60E-124 |
| 24 | cg43264442 | 199 | GGGGCGGGGT GGAGAAGCTGC GGC[AG]GGCG GCCCGTAGGAA GGTGCTGTC | A | G | SILENT- NONCODING | dehydrog enase | Human Gene TREMBLNEW- ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT (EC 1.1.1.22) - BOS TAURUS, 468 aa. | 8.60E-240 |
| 25 | cg43264442 | 236 | AGGAAGGTGCT GTCCCGAACGAT CGG[G/A]ATAGG AGGGTCCCTG CGCTTGCTG | G | A | SILENT- NONCODING | dehydrog enase | Human Gene TREMBLNEW- ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT (EC 1.1.1.22) - BOS TAURUS, 468 aa. | 8.60E-240 |
| 26 | cg43998926 | 130 | GAACCCAAGAG CCACTGATAACT GG[C/gap]ACAAT CCAATGAAACA GAGGAAGCA | C | gap | SILENT- NONCODING | dehydrog enase | Human Gene SWISSPROT- ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa. | 1.30E-190 |

| | | | | | | | | | | | |
|----|-------------|-----|--------------|---|---|--|----------------------|------------------|---|-----------|---------------------|
| 27 | cg43998926 | 560 | CTCAGGGCTGAG | T | G | | SILENT- NONCODING | dehydrg enase | Human Gene SWISSPROT- ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa. | 1.30E-190 | 15 |
| 28 | cg43941594 | 499 | GGTTATAAAAT | A | G | | SILENT- NONCODING | dehydrg enase | Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL- 3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa. | 1.90E-137 | 3 |
| 29 | cg439962927 | 462 | GCCACTCCCTG | G | A | | SILENT- NONCODING | dna_rna _bind | Human Gene SWISSPROT- ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1)- HOMO SAPIENS (HUMAN), 993 aa. | 0.00E+00 | 11 (11q13.2) |
| 30 | cg43991661 | 671 | CTTGTATTAT | C | G | | SILENT- NONCODING | dna_rna _bind | Human Gene TREMBLNEW- ID:G2058493 TELOMERIC REPEAT DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 419 aa. | 5.10E-224 | 8 |
| 31 | cg43991661 | 737 | ACTGTTTAGGC | A | G | | SILENT- NONCODING | dna_rna _bind | Human Gene TREMBLNEW- ID:G2058493 TELOMERIC REPEAT DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 419 aa. | 5.10E-224 | 8 |
| 32 | cg43310449 | 206 | CTAAAGATTCA | A | G | | SILENT- NONCODING | dynein | Human Gene SWISSPROT- ID:Q63100 DYNEIN INTERMEDIATE CHAIN 1, CYTOSOLIC (DH IC-1)- RATTUS NORVEGICUS (RAT), 643 aa. | 1.0e-312 | |
| 33 | cg43310449 | 231 | ACTGGCATACT | G | A | | SILENT- NONCODING | dynein | Human Gene SWISSPROT- ID:Q63100 DYNEIN INTERMEDIATE CHAIN 1, CYTOSOLIC (DH IC-1)- RATTUS NORVEGICUS (RAT), 643 aa. | 1.0e-312 | |

| | | | | | | | | | | |
|----|------------|------|--|---|---|--|----------------------|------------------|---|-----------|
| 34 | cg43984524 | 1227 | TCAATGAGGCCCT TCATTAAATTCC CTT/CJTAAAAGC AATGGTTTATT TGAAA | T | C | | SILENT- NONCODING | esterase | Human Gene Similar to SPTREMBL- ID:P0665 SIALIC ACID-SPECIFIC 9- O-ACTYLESTERASE - MUS MUSCULUS (MOUSE), 541 aa. | 3.2E-99 |
| 35 | cg43248101 | 2516 | GGCCCTGTGAATG TTATGAAGGTTT GA[G/A]GTCAAGC CTACAGATAACA GGATTAT | G | A | | SILENT- NONCODING | fgf | Human Gene Homologous to SWISSPROT-ID:P21781 KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR-7) (FGF-7) (HBGF-7) - HOMO SAPIENS (HUMAN), 194 aa. | 9.30E-106 |
| 36 | cg43974968 | 2973 | CAGTGGCTCAC GCCTATAATCCC AG[C/A]ACTTTG GGAGGCCAAGG CAGGAGGA | C | A | | SILENT- NONCODING | fgf | Human Gene Homologous to SPTREMBL-ID:P78443 21 KD BASIC FIBROBLAST GROWTH FACTOR (BFGF) - HOMO SAPIENS (HUMAN), 196 aa. | 1.70E-103 |
| 37 | cg43074195 | 222 | CAGCTGAAGGA GATAATTGGTGT GA[A/G]CAGAAAG CTGAAAGCTTCT AATGGAG | A | G | | SILENT- NONCODING | glycoprot ein | Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.40E-197 |
| 38 | cg43074195 | 237 | ATGGGTGTGAAC AGAACGCTGAAA GCTTAATCTAATG GAGACACTCT ACACATG | T | A | | SILENT- NONCODING | glycoprot ein | Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.40E-197 |
| 39 | cg43074195 | 246 | AACAGAACGCTG AAAGCTCTAAAT GG[A/G]GACACT CCTACACATGAA GACTTGA | A | G | | SILENT- NONCODING | glycoprot ein | Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.40E-197 |
| 40 | cg43074195 | 255 | TGAAAGCTTCTA ATGGAGACACT CC[T/A]ACACAT GAAGACTTGAC CAAGAACAA | T | A | | SILENT- NONCODING | glycoprot ein | Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.40E-197 |

| | | | | | | | | | | |
|----|------------|------|--|----------|--|----------------------|------------------|---|----------|---|
| 41 | cg43988092 | 658 | TAGCGATACAAA TATATATATAT [A/gap]TTATCC AAAAATATGTT TATACA | gap | | SILENT- NONCODING | glycoprot ein | Human Gene SWISSPROT- ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa. | 2.9E-150 | 4 |
| 42 | cg43953517 | 2457 | AAGTTCTTGTAG TAGGTAGGGGG TA[C/T]TACAGG GATACTGTGG CATGATT | C T | | SILENT- NONCODING | glycoprot ein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 43 | cg43953517 | 2464 | TGTAGTAGGTA GGGGGTACTAC TAG[G/C]GATAT CTGTGGCATGA TTATGCATT | G C | | SILENT- NONCODING | glycoprot ein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 44 | cg43953517 | 2491 | ATATCTGTGGCA TGATTATGCCATT C[C/gap]GTAGTA TTATTAAATTAA TTGGGG | C gap | | SILENT- NONCODING | glycoprot ein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 45 | cg43953517 | 2517 | GTAGTATTATT AATTAAATTGGG GT/GTCATTGG CTTCCCTTCTT TATGCC | T G | | SILENT- NONCODING | glycoprot ein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 46 | cg43953517 | 2529 | AATTAAATTGGG GTTCAATTTGCT T[C/gap]CTTTTC TTTATGCTTAGA TTATCCTT | C gap | | SILENT- NONCODING | glycoprot ein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 47 | cg43953517 | 2530 | ATTAATTTGGGG TTCAATTTGCTT C[C/gap]TTTTCT TTATGCTTAGAT TATCTTA | C gap | | SILENT- NONCODING | glycoprot ein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |

| | | | | | | | | | | | |
|----|------------|------|---|---|-----|--|----------------------|------------------|--|---------|------------------|
| 48 | cg43290087 | 1150 | CCTAACCTCTTG GTAACGGTAGT CCCT/C]GAGAGT TCGCAGTGTCA GTGAAATC | T | C | | SILENT- NONCODING | glycoprot ein | Human Gene Similar to SWISSPROT- ID:PS2166 MEMBRANE PROTEIN SEL-12 - CAENORHABDITIS ELEGANS, 461 aa. | 1.7E-97 | 14 (14q24.3) |
| 49 | cg43294632 | 913 | AGTAGAGAGTA GGGTAAAAGC TGGIAVG]CATTG CAAAGGATTG GTTAAAGAA | A | G | | SILENT- NONCODING | glycoprot ein | Human Gene Similar to SWISSNEW- ID:Q13361 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN 2 PRECURSOR (MAGP-2) (MP25) - HOMO SAPIENS (HUMAN), 173 aa. lpcis:SWISSPROT-ID:Q13361 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 2 PRECURSOR (MAGP-2) - HOMO SAPIENS (HUMAN), 173 aa. | 4.3E-92 | 12 |
| 50 | cg43056971 | 884 | GTTATTGGAAA ATACCTATTTT TT/gap]CCAAG TGTGAAAAGAT TGTTTG | T | gap | | SILENT- NONCODING | glycoprot ein | Human Gene Similar to SPTREMBL- ID:O04711 P-GLYCOPROTEIN-2- ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 1233 aa. | 2.2E-72 | 1 |
| 51 | cg43976227 | 212 | TTCATGTGCAAG CTAAGTTATTC [C/A]TGGTCAAT CCTCTCCATCTT CTGGT | C | A | | SILENT- NONCODING | glycoprot ein | Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 2.6E-60 | 18 |
| 52 | cg43994600 | 1782 | CCTTGTCCCCAC TCTCCCTTCATAT [C/T]AAGTCAT CAAACATCTGAA TGAGAG | C | T | | SILENT- NONCODING | helicase | Human Gene Similar to SWISSNEW- ID:O70133 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) (MHEL-5) - MUS MUSCULUS (MOUSE), 1380 aa. lpcis:TREMBLNEW-ID:G2961456 RNA HELICASE A - MUS MUSCULUS (MOUSE), 1380 aa. | 8.7E-67 | 14 |

| | | | | | | | | | | |
|----|------------|------|---|---|---|----------------------|----------------|---|---|---|
| 53 | cg43925670 | 2481 | ATGTTCTTGTAT TTTTTCCCATC TITCCTACAGACA TAAGTGAGCCT CACTGG | C | T | SILENT- NONCODING | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR- HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0 | 1 |
| 54 | cg43925670 | 2488 | TGTATTTTTTTC CCATCTTACAG A[C/T]ATAAGTG GCCTCACTGGA AATTAA | C | T | SILENT- NONCODING | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR- HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0 | 1 |
| 55 | cg43925670 | 2501 | CATCTTTACAGA CATAGTGAGC CTC[TACTGGA AATTTTTCAAC AGTAGTC | C | T | SILENT- NONCODING | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR- HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0 | 1 |

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|----|------------|------|---------------|---|---|------------------|---|-----------|--|---|---|
| 56 | cg43925670 | 2507 | TACAGACATAAAG | A | G | SILENT-NONCODING | n | Interfero | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0 | 1 |
| 57 | cg43925670 | 2513 | CATAAGTGAGC | T | C | SILENT-NONCODING | n | Interfero | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0 | 1 |
| 58 | cg43925670 | 2551 | CCAGATCTTGA | C | T | SILENT-NONCODING | n | Interfero | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0 | 1 |

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|----|------------|------|--|---|-----|--|----------------------|-----------------------|--|----------|-----------------|
| 59 | cg42489232 | 2434 | ATTTTAGTGA GACAAGGTTTG C[C]ATGTTGG CCAGGCTGGTC TCGAAC | C | T | | SILENT- NONCODING | interfero n | Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2)- HOMO SAPIENS (HUMAN), 515 aa. | 3.9E-281 | 21 (21q22.1) |
| 60 | cg42489232 | 2441 | GTAGAGACAAG GTTTGGCATGT TG[G]CCAGGC TGGTCTCGAACT CCTGACC | G | C | | SILENT- NONCODING | interfero n | Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2)- HOMO SAPIENS (HUMAN), 515 aa. | 3.9E-281 | 21 (21q22.1) |
| 61 | cg42489232 | 2454 | TTGCCATGTTG GCCAGGCTGGT CT[C]GAACTC CTGACCTCAAG CGATCCGC | C | T | | SILENT- NONCODING | interfero n | Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2)- HOMO SAPIENS (HUMAN), 515 aa. | 3.9E-281 | 21 (21q22.1) |
| 62 | cg43926168 | 694 | GAAGGGCTCT CTTCACGGGG CTG[A/gap]AAAA AAAAAAATCATGA AATCCTAAT | A | gap | | SILENT- NONCODING | interleuki nrecept | Human Gene Similar to SWISSPROT- ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa. | 8.8E-94 | 2 (2q14.2) |
| 63 | cg43926168 | 704 | CCTTCACGGGG ACTGAAAAAA AA[A/gap]TCATG AAATCCTAATT TCATTTTC | A | gap | | SILENT- NONCODING | interleuki nrecept | Human Gene Similar to SWISSPROT- ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa. | 8.8E-94 | 2 (2q14.2) |

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|----|------------|------|---|--------|--|----------------------|--------|--|-----------|----|
| 64 | cg43336163 | 2889 | AGCCGGAAATG CTGCTGCTGCT GCT[G]CTGCT GCTGCTGCTGC TGGGGAT | G A | | SILENT- NONCODING | Kinase | Human Gene TREMBLNEW- ID:G300258 MYOTONIC DYSTROPHY KINASE, DM-KINASE (C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II) - HOMO SAPIENS, 616 aa. | 0 | 19 |
| 65 | cg43987164 | 1043 | AGGGCAAGCCCC TCAGAAAGCCTTC CC[G]AGCAGAT CCGGGGACCCC GTTCTGGT | G A | | SILENT- NONCODING | Kinase | Human Gene TREMBLNEW- ID:D1023392 INOSITOL 1,4,5- TRISPHOSPATE 3-KINASE ISOENZYME (EC 2.7.1.127) - HOMO SAPIENS (HUMAN), 604 aa (fragment). | 1.3E-307 | |
| 66 | cg43119489 | 2227 | TTTTCATCCTA TCAATTGAATGT G[G/C]CTTGGAA AATCCAGCAAG AGGGGG | G C | | SILENT- NONCODING | Kinase | Human Gene SWISSPROT- ID:Q00537 SERINE/THREONINE- PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa. | 2.7E-282 | |
| 67 | cg43957170 | 2164 | CTACTAAAAATA CAAAAAATTAGC C[G/A]GGCGTGG TGGCGCATGCC TGTAGTC | G A | | SILENT- NONCODING | Kinase | Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa. | 1.7E-234 | |
| 68 | cg43957170 | 2175 | ACAAAAAATTAG CCGGGGTGGT GG[C/T]GCATGC CTGTAGTCCCA GCTACTCG AAAATTAGCCG | C T | | SILENT- NONCODING | Kinase | Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa. | 1.70E-234 | |
| 69 | cg43957170 | 2179 | GGCGTGGTGGC GCA[T]GCCCTG TAGTCCAGCTA CTCGGAG | T C | | SILENT- NONCODING | Kinase | Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa. | 1.70E-234 | |

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|----|------------|------|---|-----|--|----------------------|--------|---|-----------|----|
| 70 | cg38438124 | 1767 | ACCTTGTGATA G TCTGTGTGTT GT[G/gap]TGTG GGGGGGTGA GTGTGTGCG | gap | | SILENT- NONCODING | kinase | Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa. | 2.80E-216 | 10 |
| 71 | cg38438124 | 1769 | TTTGTATATG G TGTGTGTGTT GT[G/gap]TGGG GGGGGTGAGT GTGTGCGCG | gap | | SILENT- NONCODING | kinase | Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa. | 2.80E-216 | 10 |
| 72 | cg42923882 | 123 | AGTGGGCAGGG C ACCCCTGGAGC CTC/C/AATTCTC AATGCCACC CTTTACCT | A | | SILENT- NONCODING | kinase | Human Gene SPTREMBL-ID:Q92961 MAP KINASE KINASE MEK5B - HOMO SAPIENS (HUMAN), 448 aa. | 1.80E-196 | |
| 73 | cg43948037 | 1031 | AAAGTTCTCGAA G ATGCTTCATCCC C[G/A]ACAAAGC AAATTTCATGTC CGTCAG | A | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KKIAIRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 | |
| 74 | cg43948037 | 1106 | CTGTTGCTTCC G CTGGGGTGTCC AG[G/A]CTCACC AGGGAGTCAG AATCTCT | A | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KKIAIRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 | |

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|----|------------|------|---|----------|--|----------------------|--------|--|-----------|
| 75 | cg43948037 | 1115 | TCCCTGGGTG TCCAGGCTCAC CAG[G/C]GGAGT CAGAACCTCTG GTTCTCCC | G C | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KK1ALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 |
| 76 | cg43948037 | 1124 | TGTCCAGGCTC ACCAGGGAGT CAGIA[GATCTT CTGGTCTCCCT TTTCATCA | A G | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KK1ALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 |
| 77 | cg43948037 | 1134 | CACCAAGGGGAG TCAGAA[TCTTCT GGT]CTCTCCC TTTCATCAAGT CTTCTAA | T C | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KK1ALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 |
| 78 | cg42703622 | 2409 | TGTGGGGTTGAC AGATTTTAAAA TA[G]CAATTAG AGATTTTGGGT TTTGTT | G C | | SILENT- NONCODING | kinase | Human Gene SPTRMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa. | 3.00E-187 |
| 79 | cg43336176 | 5568 | TGCTGCTGGCTG CTGCTGCTGGG GGG[gap]ATCA CAGACCATTTCT TTCTTCGG | G gap | | SILENT- NONCODING | kinase | Human Gene SPTRMBL-ID:Q16205 MYOTONIN PROTEIN KINASE - HOMO SAPIENS (HUMAN), 625 aa. | 1.10E-164 |
| 80 | cg43982923 | 610 | ACGCAGGGTC CCGGGGCGC CGC[G/A]ATGCA GAAA[ACGAGA AACTGGAAA | G A | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa. | 3.60E-159 |

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|----|------------|------|--------------|---|---|--|----------------------|----------------|---|-----------|----|
| 81 | cg43265203 | 688 | ACATTCAAGCTC | A | C | | SILENT- NONCODING | Kinase | Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.[pcis:SWISSPROT-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.] | 5.50E-124 | |
| 82 | cg43966625 | 77 | CGCTGCCGG | A | C | | SILENT- NONCODING | Kinase | Human Gene Similar to SWISSPROT-ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) [PYRUVATE DEHYDROGENASE KINASE ISOFORM 2] - HOMO SAPIENS (HUMAN), 407 aa.[pcis:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.] | 3.20E-89 | 17 |
| 83 | cg44004317 | 4772 | CACCCGATGC | G | A | | SILENT- NONCODING | Kinasereceptor | Human Gene SWISSNEW-ID:P04626 ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (P185ERBB2) (NEU PROTO-ONCOGENE) (C-ERBB-2) - HOMO SAPIENS (HUMAN), 1255 aa.[pcis:SWISSPROT-ID:P04626 ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1255 aa.] | 0.00E+00 | |
| 84 | cg43925424 | 300 | TCGGCGCACAG | G | T | | SILENT- NONCODING | Kinesin | Human Gene SWISSPROT-ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa. | 1.90E-304 | 14 |

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|----|------------|------|--------------|---|---|--|------------------|--------------|--|-----------|----|
| 85 | cg44002977 | 242 | TAGGGACCAC | G | A | | SILENT-NONCODING | kinesin | Human Gene Similar to SWISSPROT-ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa. | 2.70E-60 | 6 |
| 86 | cg27803682 | 2540 | TTGAGCCTCCA | G | A | | SILENT-NONCODING | misc_channel | Human Gene Similar to SPTREMBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN-CAENORHABDITIS ELEGANS, 461 aa. | 3.50E-81 | |
| 87 | cg43971768 | 2349 | GAACTGCAGTC | A | G | | SILENT-NONCODING | nucl_rec pt | Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa. | 0.00E+00 | 15 |
| 88 | cg43987181 | 1358 | AAGCTTAGTACT | T | A | | SILENT-NONCODING | nucl_rec pt | Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE)(EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (IP54) (FF1 ANTIGEN)- HOMO SAPIENS (HUMAN), 457 aa. pcds:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE)(EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (IP54) (FF1 ANTIGEN)- HOMO SAPIENS (HUMAN), 457 aa. | 9.40E-248 | 6 |

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| 89 | cg43263644 | 143 | GCCGGGACAGT GTTGTACAGTGT TTT/CIGGGCAT GCACGTGATAC TCACACAG | T | C | SILENT- NONCODING | nucL_rec pt | Human Gene SWISSPROT- ID:Q03181 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA) (PPAR-DELTA) (NUCLEAR HORMONE RECEPTOR 1) (NUC1) (NUC1) - HOMO SAPIENS (HUMAN), 441 aa. |
| 90 | cg44131079 | 3497 | CGGTGATATTAC AAAACAATGAAT TC[T]GGAACAT TATAGATTGGGC ACCTC | C | T | SILENT- NONCODING | nuclease | Human Gene SWISSPROT-ID:P10266 RETRORVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]- HOMO SAPIENS (HUMAN), 874 aa. Ipcis:SWISSPROT-ID:P10266 RETRORVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC.2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. |
| 91 | cg44031914 | 153 | GCACAGGGAG TGAGGGCAGGG CGCT[C]CGCAG GGGGCACGCAG GGAGGGCCC | T | C | SILENT- NONCODING | oncogen e | Human Gene SWISSPROT- ID:Q01543 FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR) - HOMO SAPIENS (HUMAN), 452 aa. |
| 92 | cg43932550 | 3136 | CATCATAGAACT CCTTGTTGGATCT C[G]ATAGAGCT CAGGGACTTG AAGAAGA | G | A | SILENT- NONCODING | oncogen e | Human Gene SPTREMBL-ID:Q13746 BCR-ABL mRNA OF ACUTE LYMPHOCYTIC LEUKAEMIA (ALL) PATIENTS - HOMO SAPIENS (HUMAN), 386 aa. |
| 93 | cg43932550 | 3312 | GACAGGACCCA TTTTCTCATCTC CA[A]G[G]CCCT TTCCAAGTCCAG CTCACTC | A | G | SILENT- NONCODING | oncogen e | Human Gene SPTREMBL-ID:Q13746 BCR-ABL mRNA OF ACUTE LYMPHOCYTIC LEUKAEMIA (ALL) PATIENTS - HOMO SAPIENS (HUMAN), 386 aa. |

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|----|------------|------|---|----------|--|----------------------|-----------------|--|-----------|
| 94 | cg43967268 | 598 | ACGGAGAAAGG AGCAGCTGAAA GTG[G/A]CCCTGG ACTCCAGCCCT GGCTGTTGT | G A | | SILENT- NONCODING | oncogen e | Human Gene Similar to SWISSPROT- ID:P24407 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 207 aa. | 1.90E-52 |
| 95 | cg43920534 | 1076 | CGTCACTATGTA CTTGGTTTGC CTT/gapTTTTTT CCTTAAAAAAA AAGGCC | T gap | | SILENT- NONCODING | phosphat ase | Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT)- RATTUS NORVEGICUS (RAT), 976 aa. | 0.00E+00 |
| 96 | cg43920534 | 763 | CTTCATAAAACC AATCGAGAGAG AG[A]gap]GGACT AAAAATCCGTCT TACCAAAA | A gap | | SILENT- NONCODING | phosphat ase | Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT)- RATTUS NORVEGICUS (RAT), 976 aa. | 0.00E+00 |
| 97 | cg43926887 | 1786 | ATTGTTTCAAC ATGAAGTAAAGA ATT[A]AACGTTGA GGCCTTACTAT TAGCT | T A | | SILENT- NONCODING | phosphat ase | Human Gene SWISSPROT- ID:Q06190 PROTEIN PHOSPHATASE PP2A, 130 KD REGULATORY SUBUNIT (PR130) - HOMO SAPIENS (HUMAN), 1150 aa. | 0.00E+00 |
| 98 | cg43926887 | 1838 | GTCTAATACTCC TGGGAGGAAGG AA[T/A]ATATCTA TCTAGTAAGAAT TTTAAT | T A | | SILENT- NONCODING | phosphat ase | Human Gene SWISSPROT- ID:Q06190 PROTEIN PHOSPHATASE PP2A, 130 KD REGULATORY SUBUNIT (PR130) - HOMO SAPIENS (HUMAN), 1150 aa. | 0.00E+00 |
| 99 | cg43088901 | 2303 | GAGCACCGTGT CAAGCTGCTCT GAGIC[T]CACAG TGGGATGAACC AGCCGGGGC | C T | | SILENT- NONCODING | phosphat ase | Human Gene SWISSNEW-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa Ipcls: SWISSPROT-ID:P30304 M- PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa. | 4.00E-288 |

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|-----|------------|------|---|---|-----|--|----------------------|--------------------------|---|-----------|----|
| 100 | cg43920213 | 3664 | GTGAGCCATAAT ATGATGGCCAG CA[G/gap]GTGG CGCTGCCCTCC ACCCATGGTG | G | gap | | SILENT- NONCODING | phosphat ase | Human Gene Similar to SWISSPROT- ID:P51452 DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR) - HOMO SAPIENS (HUMAN), 185 aa. | 6.00E-81 | 17 |
| 101 | cg43969348 | 648 | TGGGGAAATG GGCCTCTGGG GGT[C/gap]TCAC TGCACGGCTTG TTCATGGCA | C | gap | | SILENT- NONCODING | polymera se | Human Gene Similar to SPTREMBL- ID:Q15370 RNA POLYMERASE II TRANSCRIPTION FACTOR SII P18 SUBUNIT - HOMO SAPIENS (HUMAN), 118 aa. | 3.90E-59 | 16 |
| 102 | cg43966692 | 331 | TACGAATTGGCA TATTGTTTATT [C/gap]TCAGTT GTGAAAATGTCC TTAATT | C | gap | | SILENT- NONCODING | polymera se | Human Gene Similar to SPTREMBL- ID:Q15369 RNA POLYMERASE II ELONGATION FACTOR SII, P15 SUBUNIT - HOMO SAPIENS (HUMAN), 112 aa. | 4.00E-57 | 8 |
| 103 | cg43265754 | 4375 | CGAGACCAGCC TGGCCAACATG GTG[A/C]AACCC CATCTCTACTAA AAATACAA | A | C | | SILENT- NONCODING | potassi m_chann el | Human Gene SWISSPROT- ID:P48544 G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 4 (GIRK4) (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 5) (HEART KATP CHANNEL) (KATP-1) (CARDIAC INWARD RECTIFIER) (CIR) (KIR3.4) HOMO SAPIENS (HUMAN), 419 aa. | 6.70E-185 | |
| 104 | cg43265754 | 4389 | CCAACATGGTG AAACCCATCTC TA[C/T]AAAAAT ACAAAAAATTAGC CGGGCG | C | T | | SILENT- NONCODING | potassi m_chann el | Human Gene SWISSPROT- ID:P48544 G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 4 (GIRK4) (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 5) (HEART KATP CHANNEL) (KATP-1) (CARDIAC INWARD RECTIFIER) (CIR) (KIR3.4) HOMO SAPIENS (HUMAN), 419 aa. | 6.70E-185 | |

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|-----|------------|------|--|----------|--|----------------------|---------------|--|-----------|---------------------|
| 105 | cg43922227 | 538 | ATGTTGTGGC GCCAGATT CC[C/T]ATTGAT TTCTTGCATCA TTTCT | C T | | SILENT- NONCODING | reductas e | Human Gene Homologous to SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa. | 7.70E-150 | 14 |
| 106 | cg43927549 | 1020 | GTAAGCAGCAC ACTAGGAGGCC CAG[G/gap]CGC AGGAAAGAGA AGATGGTGCTG | G gap | | SILENT- NONCODING | reductas e | Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE)- HOMO SAPIENS (HUMAN), 231 aa. | 1.60E-124 | 6 (6pter) |
| 107 | cg43957486 | 4041 | TGTATCATGAA ATGTAACCTTG T[A/G]AGACAAA GGTTTTCCTCTT CTATTT | A G | | SILENT- NONCODING | struct | Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa. | 0.00E+00 | 20 (20p11.2) |
| 108 | cg43973080 | 779 | GACACTAGGAA TTTCTTAAAAAG AA[A/gap]GATGT TGGAAAGCAGAA CACTTACTA | A gap | | SILENT- NONCODING | struct | Human Gene TREMBLNEW- ID:G2304981 MYOSIN VI - HOMO SAPIENS (HUMAN), 1262 aa. | 0.00E+00 | 6 |
| 109 | cg42914441 | 2306 | CTCTGACCTGA GTCCTTGTATA AG[A/G]AGTATT GTCCTTCTTTGT CTAATG | A G | | SILENT- NONCODING | struct | Human Gene Homologous to SWISSPROT-ID:P26044 RADIXIN (MOESIN B) - SUS SCROFA (PIG), 583 aa. | 5.40E-133 | 22 (22q12.2) |
| 110 | cg43942318 | 1006 | GGACACCCCTCG GACCCCTCGAAA ACGIC[TCTCAG GAGCTATGAAG ACATGATTG | C T | | SILENT- NONCODING | struct | Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa. | 4.80E-123 | 11 |

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|-----|------------|------|--|----------|--|----------------------|----------|---|-----------|----|
| 111 | cg43929933 | 431 | CAGGCCAGGCC TGTGTGCCAC CTG[G]ACAGG CATTCCCTTG TCCAGAAA | C G | | SILENT- NONCODING | struct | Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa. | 1.80E-117 | 12 |
| 112 | cg43929933 | 541 | CGCAGCCCCAA GTGTCAAACAG GGG[C/T]TCAAAT AAGGCCTTCTG GGAGCCACT | C T | | SILENT- NONCODING | struct | Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa. | 1.80E-117 | 12 |
| 113 | cg43929933 | 590 | CTGGCAGCTGG TGGGATGGAAAG GGG[G/g]AGG TGGAAAAGGGC AGAGGAAATGG | G gap | | SILENT- NONCODING | struct | Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa. | 1.80E-117 | 12 |
| 114 | cg43070037 | 7268 | AGGTCAGGAGT TTGAGGACCAAGC CTA[G/A]CCAAC ATGGTGAACC CCATCTTA | G A | | SILENT- NONCODING | Synthase | Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGLASTER (FRUIT FLY), 1354 aa. | 0.00E+00 | |

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| 115 | cg43070037 | 7269 | GGTCAGGAGT | C | G | | SILENT-NONCODING | synthase | Human Gene SWISSPROT-ID:P35421 | 0.00E+00 |
| | | | TGAGACCAGCC TAG[C/G]CAACA TGGTAAACCC CATCTCTAC | | | | | | PHOSPHORIBOSYLFORMYLGLYCINAMIDE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa. | |
| 116 | cg43070037 | 7352 | GTGGGTGCCTG | C | T | | SILENT-NONCODING | synthase | Human Gene SWISSPROT-ID:P35421 | 0.00E+00 |
| | | | TAATCCCAGCTA CTC/TGGGAGG CTGAGGCAGGA GAATCACC | | | | | | PHOSPHORIBOSYLFORMYLGLYCINAMIDE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa. | |
| 117 | cg43070037 | 7365 | ATCCCCAGCTACT | C | T | | SILENT-NONCODING | synthase | Human Gene SWISSPROT-ID:P35421 | 0.00E+00 |
| | | | CGGGAGGCTGA GGC/TJAGGAGA ATCACCTGAAC TAGGAGG | | | | | | PHOSPHORIBOSYLFORMYLGLYCINAMIDE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa. | |

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| 118 | cg43070037 | 7366 | TCCCCAGCTACTCA GGGAGGCTGAG GC[A/G]GGAGAA TCACCTGAACCT AGGAGGC | A | G | SILENT- NONCODING | synthase | Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGLASTER (FRUIT FLY), 1354. aa. | 0.00E+00 |
| 119 | cg43123664 | 240 | AGTAGGCCAGC CGGGGGGCC CCG[A/C]ATGTA CATGTTCCACG CGGGATTCC | A | C | SILENT- NONCODING | synthase | Human Gene Similar to SWISSPROT- ID:O35696 ALPHA-2.8- SIALYLTRANSFERASE (EC 2.4.99.-) (ST8SIAII) (SIALYLTRANSFERASE X) (STX) (POLYSIALIC ACID SYNTHASE) - MUS MUSCULUS (MOUSE), 375. aa. | 3.10E-59 |
| 120 | cg21428405 | 17 | NACGGTTGGC GTCGT[C]CTC GTTGAGCTCATC AATCCACAC | T | C | SILENT- NONCODING | synthase | Human Gene Similar to SWISSPROT- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754. aa. | 2.20E-56 |
| 121 | cg43982633 | 811 | ACACAGCCCCA GTTTGCTTACA GC[C/G]CAAGTT ACAAACTGTCCC TTTAAAAA | C | G | SILENT- NONCODING | tgfrceptor or | Human Gene SWISSPROT- ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR- ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464. aa. | 1.50E-254 |
| 122 | cg43054268 | 312 | TCTAGATATTA ACTGACCCACTA T[Agap]TTCCCTC AAGGATACTGCA ATTTGGAC | A | gap | SILENT- NONCODING | thioester ase | Human Gene Similar to TREMBLNEW-ID:E307161 MITOCHONDRIAL VERY-LONG- CHAIN ACYL-COA THIOESTERASE - RATTUS NORVEGICUS (RAT), 453 aa. | 3.50E-83 |

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|-----|------------|------|--|----------|--|----------------------|------------------|---|-----------|----------|
| 123 | cg43054268 | 448 | GAATATGATC AAAGCCTTATG C[A]gap[AAAAAA ATTTTTAATT TGCAAA | A gap | | SILENT- NONCODING | thioester ase | Human Gene Similar to TREMBLNEW-ID:E307161 MITOCHONDRIAL VERY-LONG- CHAIN ACYL-COA THIOESTERASE RATTUS NORVEGICUS (RAT), 453 aa. | 3.50E-83 | 9 |
| 124 | cg43943775 | 259 | TGAAGATTACCC CCACACCTGTG TG[A/G]CAAGTG ATCAAAAAGGAA CAGGACC | A G | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P21554 CANNABINOID RECEPTOR 1 (CB1) (CB-R) (CANIN6) -HOMO SAPIENS (HUMAN), 472 aa. | 5.40E-252 | 6 (6q14) |
| 125 | cg42886565 | 3473 | GGCAACAAAAAG CGAAAACCTCCATC TC[A]gap[AAAAAA AAAGAGCTATAG GATCTTA | A gap | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa. | 4.40E-225 | 5 (5q13) |
| 126 | cg42886565 | 3481 | AAGCGAAACTC CATCTCAAAAAA AA[A]gap[GAGCT ATAGGATCTTTA CAATATA | A gap | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa. | 4.40E-225 | 5 (5q13) |
| 127 | cg42886565 | 4462 | TCCCTGTCTGC TGGCTGCCGC GT[G/A]TATGAA GAAGACTAAATTG GACACAG | G A | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa. | 4.40E-225 | 5 (5q13) |
| 128 | cg42886565 | 4483 | GCGTGTATGAA GAAGACTAAATTG GA[C/T]ACAGAG CCGTGATGAATT AAAGTCT | C T | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa. | 4.40E-225 | 5 (5q13) |
| 129 | cg43307001 | 1796 | GCCTCCGGGT TCAAGTGATTCT CC[T/C]GCCCTCA GCCTCCAGTA GCTGGGAT | T C | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa. | 2.50E-199 | |

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| 130 | cg43307001 | 1898 | GGGGTTTCAACC ATGTTGGCCAG GCT[G/A]GTCTC GAACCTCCGTAC CTCAAGTGA | G A | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa. | 2.50E-199 | |
| 131 | cg43307001 | 1909 | ATGTTGGCCAG GCTGGTCTCGA ACT[C/T]CTGAC CTCAAGTGATCC GCCACCT | C T | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa. | 2.50E-199 | |
| 132 | cg43047341 | 2113 | GGTGGATCACC TGAGGTCACTGA GTT[C/T]GAGAC CAGCCTGACCA ACATGGAGA | C T | gap | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P21731 THROMBOXANE A2 RECEPTOR (TXA2-R) (PROSTANOID TP RECEPTOR)- HOMO SAPIENS (HUMAN), 369 aa. | 2.80E-190 | |
| 133 | cg43965652 | 891 | TCCATTTCCTTT TCTTTTTTTTT [T/gap]TAAGTGA GACTACATTGG CAAATGG | T | | SILENT- NONCODING | tnf | Human Gene Homologous to SPTREMBL-ID:Q999732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa. | 4.50E-121 | 16 |
| 134 | cg43965652 | 892 | CCATTTCTTTTT CTTTTTTTTT [T/gap]AAGTGA ACTACATTGGCA AATGGG | T | gap | SILENT- NONCODING | tnf | Human Gene Homologous to SPTREMBL-ID:Q999732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa. | 4.50E-121 | 16 |
| 135 | cg43965652 | 412 | TTCCAACATCA AATGAAGGGGG AT[C/gap]AATGG TTACCACTATCG TTTCAAC | C G | gap | SILENT- NONCODING | tnf | Human Gene Homologous to SPTREMBL-ID:Q999732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa. | 4.50E-121 | 16 |
| 136 | cg43985709 | 933 | AGCTCACTTTGG CCCTTCTCCACC CAGTCCCCAAC CCCATTGCTAAC AACATG | A G | | SILENT- NONCODING | tnf | Human Gene Similar to SWISSPROT- ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa. | 1.70E-51 | 16 |

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| 137 | cg44027791 | 1118 | GCCACAGGGCT G CCTTTCACCCAG G[G/gap]CCCA GGAGGACACA GGTGGGGAC | gap | | SILENT- NONCODING | transcript factor | Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa. |
| 138 | cg44027791 | 1173 | TCTTCAGGGCC G TCCCGCCGCAG TTG[G/A]CCTTA CAAGTTCTTCGT GACCAGGT | A | | SILENT- NONCODING | transcript factor | Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa. |
| 139 | cg44027791 | 916 | AAGGGGTTCCCCA G CGCGTCCCTGGT TTA[G/A]AACGT CTCATGGGCA CGGCCAGTG | A | | SILENT- NONCODING | transcript factor | Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa. |
| 140 | cg44027791 | 930 | GTCCCTGGTTAG G AACGTCTCATGG G[G/gap]CACGG CCAGTGTCCAC AGTCTGGGC | gap | | SILENT- NONCODING | transcript factor | Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa. |
| 141 | cg43984418 | 923 | TATGCAATGTTCT AGCATTTTTT T[T/gap]TCACAG CACTAGAGACC CTGTTAAA | T | gap | SILENT- NONCODING | transcript factor | Human Gene SWISSPROT- ID:P23771 TRANS-ACTING T-CELL SPECIFIC TRANSCRIPTION FACTOR GATA-3 - HOMO SAPIENS (HUMAN), 443 aa. |
| 142 | cg43984418 | 937 | CATTTTTTTTT CACAGCACTAG A[G/A]ACCTGT TAAATAGGGAT ATGAGT | G | A | SILENT- NONCODING | transcript factor | Human Gene SWISSPROT- ID:P23771 TRANS-ACTING T-CELL SPECIFIC TRANSCRIPTION FACTOR GATA-3 - HOMO SAPIENS (HUMAN), 443 aa. |
| 143 | cg43945210 | 543 | CAGACAGACAC T AAGGTCTTTT TTT[G/gap]GTTTG TTTGTCCCC TCGCCAAC | T | gap | SILENT- NONCODING | transcript factor | Human Gene SWISSPROT- ID:Q60632 COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)- MUS MUSCULUS (MOUSE), 422 aa. |

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| 144 | cg43917396 | 915 | TAGGGCTGAA ACGCAGTCGG GCC[G/gap]GGC ACTGCCAGGA AGGGACTCCGG | G gap | | SILENT- NONCODING | transcript factor | Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5. HOMO SAPIENS (HUMAN), 518 aa. | 6.90E-68 |
| 145 | cg43949162 | 510 | TAGACAATACCA TCTCTAGGAACA C[A/G]CTGTAC TCACACATGGAT GTGTTG | A gap | | SILENT- NONCODING | transferase | Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa. | 1.30E-115 |
| 146 | cg41653463 | 2407 | TGTGCGTGCCT GTGTGTGTGT TGT[G/gap]GTGA TCGTGTGTGT GTTTTGTTT | G gap | | SILENT- NONCODING | transport | Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE-DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa. | 0.00E+00 |
| 147 | cg41653463 | 2408 | GTGCGTGCCT TGTGTGTGT GTGT[G/gap]GTAT CGTGTGTGT GTTTTGTTT | T gap | | SILENT- NONCODING | transport | Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE-DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa. | 0.00E+00 |
| 148 | cg43285429 | 388 | CCCAGTCAAAGA TAAGGGGGATC CCA[G/A]CAGCT CCCCCTCCGAGG TTGGGCTCT | G A | | SILENT- NONCODING | transport | Human Gene SWISSNEW-ID:P02730 BAND 3 ANION TRANSPORT PROTEIN (ANION EXCHANGE PROTEIN 1) (AE 1) - HOMO SAPIENS (HUMAN), 911 aa pcis:SWISSPROT-ID:P02730 BAND 3 ANION TRANSPORT PROTEIN (ANION EXCHANGE PROTEIN 1) (AE 1) - HOMO SAPIENS (HUMAN), 911 aa. | 0.00E+00 |
| 149 | cg43918636 | 3322 | AGCAGCAGCTG TTGGAGTAGAA CCG[C/A]GTCCA GGGCCGACCA TCTTCATCG | C A | | SILENT- NONCODING | transport | Human Gene Similar to SWISSPROT- ID:Q15012 GOLGI 4- TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108)- HOMO SAPIENS (HUMAN), 233 aa. | 5.40E-52 |

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| 150 | cg44005525 | 721 | TAAGCAGCTCTCA TTCTGTGACAGA C[A/gap]AATCAT GTAAGAACTGT GAAACCCC | A | gap | | SILENT- NONCODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN- CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |
| 151 | cg44005525 | 743 | GACAATCATGT AAGAACTGTGAA A[C/A]CCAGTT TATGTAGCGTAT CTCTTG | C | A | | SILENT- NONCODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN- CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |
| 152 | cg40986905 | 3075 | ATTTTAGTAGA GACGGGGTTTC AC[C/T]GTGTTA GCCAGGATGGT CTCGATCT | C | T | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene SPTRMBL- ACC:Q14162 KIAA0149 PROTEIN - HOMO SAPIENS (HUMAN), 830 aa. | 0.00E+00 |
| 153 | cg43303871 | 1999 | AATAAGGGAGA ACTACTATTTT TT[gap]TAAAGAT CTCAAAAATAATT AATAAA | gap | T | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene TREMBL NEW- ACC:BAA25444 KIAA0518 PROTEIN - HOMO SAPIENS (HUMAN), 650 aa (fragment). | 0.00E+00 |
| 154 | cg43303871 | 1999 | AATAAGGGAGA ACTACTATTTT TT[gap]TAAAGAT CTCAAAAATAATT AATAAA | gap | T | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene TREMBL NEW- ACC:BAA25444 KIAA0518 PROTEIN - HOMO SAPIENS (HUMAN), 650 aa (fragment). | 0.00E+00 |
| 155 | cg43918386 | 3972 | CTTCTAACCCAT GGGTAAATGTAT T[T/C]ACATATTA CCAAGAGAAGA AGCACA | T | C | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene SPTRMBL- ACC:Q14511 ENHANCER OF FILMMENTATION 1 - HOMO SAPIENS (HUMAN), 834 aa. | 0.00E+00 |
| 156 | cg43923712 | 501 | AGGAATCCCTGG ACAGGAGTTTC TG[C/T]AGAGGC GTTTAAACCCCT ACCGAAT | C | T | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene SPTRMBL- ACC:Q12996 CLEAVAGE STIMULATION FACTOR 77KDA SUBUNIT - HOMO SAPIENS (HUMAN), 717 aa. | 0.00E+00 |

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| 157 | cg43936083 | 189 | GCTAACTGGTG ACAGTTAAAAA AC[A/G]AAAAAA GGAGCCTGGGA AACAGCAA | A | G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTRMBL- ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa. | 0.00E+00 | |
| 158 | cg43936393 | 382 | AAAACAAGTTT CAGTAAAAAA A[A/gap]ACTAAA ACAAAACACTGAA GTAGAGT | A | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR- ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa. | 0.00E+00 | 17 |
| 159 | cg43936393 | 383 | AAAACAAGTTTC AGTAAAAAAA A[A/gap]CTAAA CAAAACACTGAA GTAGAGTT | A | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR- ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa. | 0.00E+00 | 17 |
| 160 | cg43940465 | 304 | ACTGTATTATT ATTTACATGGGC T[G/A]AAAGCAA AGAAAAATGAGT CCCTTC | G | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTRMBL- ACC:O60300 KIAA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment). | 0.00E+00 | |
| 161 | cg43940880 | 10186 | TAGTTGTAAGA ACTGTACAAAAA A[A/gap]TGCTTC TGGAGATTCTT TGGCAGA | A | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P53794 SODIUM/MYO- INOSITOL COTRANSPORTER (NA(+)/MYO-INOSITOL COTRANSPORTER) - Homo sapiens (Human), 718 aa. | 0.00E+00 | 21 |
| 162 | cg43950657 | 1956 | TTGGGATCCTG ATCAATTCTTC T[G/A]ATGTTGTT GAAAATGACAAA GTTGG | G | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOHA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa. | 0.00E+00 | 21 (21q22.1) |

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|-----|------------|------|---|----------|--|----------------------|------------------|--|----------|-----------------|
| 163 | cg43950657 | 2033 | CAGCTGCCAAA ACCGTGTGCA AAG[A]GGCGG ACCTAACGGGA CATTCTTG | A G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa. | 0.00E+00 | 21 (21q22.1) |
| 164 | cg43973740 | 485 | TGAAGCAAACAA ACAAACAAAAAA A[AVgap]GGAGAG CTTCATTAGTAG CCAAGAT | A gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa. | 0.00E+00 | 16 (12q12) |
| 165 | cg43980521 | 1011 | GCGCATGGTC CCTCCAGGAAG GCTTGIGGTTA GAGTCCCAGGG TGGCCCCA | T G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:BAA20795 KIAA0337 PROTEIN HOMO SAPIENS (HUMAN), 1510 aa. | 0.00E+00 | 11 |
| 166 | cg43980521 | 551 | CCCTCAGCTTGC GGGGGTCCCTC CT[G]AAAGGGG CTTCCCTGGCA GAAGGGG | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:BAA20795 KIAA0337 PROTEIN HOMO SAPIENS (HUMAN), 1510 aa. | 0.00E+00 | 11 |
| 167 | cg43980521 | 873 | AGCATCTTGATC TAGAGGACTGA GG[G/A]CAGCCC CATCAGGCTGG GGCCCTGG | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:BAA20795 KIAA0337 PROTEIN HOMO SAPIENS (HUMAN), 1510 aa. | 0.00E+00 | 11 |
| 168 | cg44019839 | 3287 | AGCTAACAGA GGAAATAACTTA GGTTCACTTCT GTTTTTTAAA AAAATA | T C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q99743 NEURONAL PAS DOMAIN PROTEIN 2 (NEURONAL PAS2) (MEMBER OF PAS PROTEIN 4) (MOP4) - Homo sapiens (Human), 824 aa. | 0 | 0 |

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|-----|------------|------|--|--------|--|----------------------|------------------|--|----------|---|
| 169 | cg44021891 | 787 | AGAAGGACCTGG CTTCCCTTACAAC AG[G/A]GACAGG CTGGTGGCTGG GGCTAGAG | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa. | 0 | 3 |
| 170 | cg44021891 | 869 | GCCCCCAGCTA GGACCCCTGTAG TTG[G/A]GACCCG TGGCATGATACA AGGACCTG | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa. | 0 | 3 |
| 171 | cg44921773 | 2876 | TTCTGAGACAG GGTCCTTGCTCT GTC[G/A]CCCCAG GCTGGAGTGCA ATGGCACGGA | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13471 REPLICATION CONTROL PROTEIN 1 - HOMO SAPIENS (HUMAN), 861 aa. | 0 | 1 |
| 172 | cg44921773 | 2955 | GGGCTCAAGTG ATCCTCCCCACT CA[A/G]CCTCCC GAGTAGCTGAG ACTACAGG | A G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13471 REPLICATION CONTROL PROTEIN 1 - HOMO SAPIENS (HUMAN), 861 aa. | 0 | 1 |
| 173 | cg43961485 | 650 | GGTCTCCTCAG TGGCTCTATTATA GGT[G/G]GTGGTT TTTTTTTTTT TTACTG | T G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60398 TXBP151 - HOMO SAPIENS (HUMAN), 563 aa. | 1.5E-303 | 7 |
| 174 | cg43985955 | 2111 | GAGCACAGATA CAGTTTATGAA CTT[A]GATGGA AGAAAATGGAAT TACTCCA | T A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.7E-299 | |
| 175 | cg44916647 | 1142 | GCTCAGCAGCC CCTAGGAAGTTA AG[C/T]GAGAGC TACAGGGCAGG GGGCCTCC | C T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa. | 4.3E-299 | 1 |

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|-----|------------|------|--------------|---|-----|----------------------|------------------|--|----------|----|
| 176 | cg44916647 | 494 | TCTGTACATGTA | C | gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75057 KIAA0469 PROTEIN- HOMO SAPIENS (HUMAN), 539 aa. | 4.3E-299 | 1 |
| 177 | cg44021459 | 2082 | GGTCACTGTTCT | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC: AAC16046 FIP2 - HOMO SAPIENS (HUMAN), 577 aa. | 1E-297 | |
| 178 | cg43926814 | 372 | TAGAAATTCTA | C | T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC: Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA- 62) - Homo sapiens (Human), 536 aa. | 5E-289 | 14 |
| 179 | cg43926814 | 412 | GTAGTGGCTGG | T | C | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC: Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA- 62) - Homo sapiens (Human), 536 aa. | 5E-289 | 14 |
| 180 | cg43931431 | 1415 | AGCCATGTAC | A | T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC: Q14154 HYPOTHETICAL PROTEIN KIAA0141 - Homo sapiens (Human), 515 aa. | 7.2E-281 | 5 |
| 181 | cg44031765 | 277 | ATGCCACCTGGC | G | A | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC: Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa. | 4.6E-279 | 22 |
| 182 | cg44031765 | 4030 | CATCTTATAGG | C | T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC: Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa. | 4.6E-279 | 22 |

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|-----|------------|------|--------------|---|-----|--|----------------------|------------------|--|-----------|----|
| 183 | cg43970492 | 331 | TGCTTTGTTGCT | A | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa. | 3.60E-270 | 22 |
| 184 | cg42847874 | 1118 | ACAAAAATTAGC | G | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA34492 KIAA0772 PROTEIN - HOMO SAPIENS (HUMAN), 468 aa. | 6.30E-258 | 20 |
| 185 | cg43951020 | 534 | GAGTGCAGTGG | C | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O76021 PBK1 PROTEIN - HOMO SAPIENS (HUMAN), 516 aa. | 6.60E-255 | |
| 186 | cg43951020 | 552 | CAACCTCCGCC | A | G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O76021 PBK1 PROTEIN - HOMO SAPIENS (HUMAN), 516 aa. | 6.60E-255 | |
| 187 | cg43971614 | 2720 | ACCATTGCTTTG | G | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 5.30E-253 | 5 |
| 188 | cg43971614 | 2802 | CTCTGGACCCAC | T | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 5.30E-253 | 5 |
| 189 | cg43962954 | 192 | CGGGCTCCCCA | C | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa. | 4.80E-252 | 19 |

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|-----|------------|------|--------------|---|-----|----------------------|------------------|--|-----------|----|
| 190 | cg43917689 | 1684 | AGGCAAACACCT | C | T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa. | 3.50E-240 | 3 |
| 191 | cg43916785 | 2176 | TCAGATGACTTT | T | C | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC: AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment). | 2.50E-230 | 14 |
| 192 | cg43287642 | 307 | GCAACTTATTG | G | A | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC: AAD20347 NEBULIN - HOMO SAPIENS (HUMAN), 977 aa (fragment). | 3.50E-224 | |
| 193 | cg43986954 | 1072 | AGTGGAAACATT | T | C | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC: AAC68871 METHYL-CPG BINDING PROTEIN MBD2 - HOMO SAPIENS (HUMAN), 411 aa. | 9.40E-224 | 18 |
| 194 | cg42882543 | 3078 | TCCCCGAGTAGC | T | C | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC: O75177 KIAA0693 PROTEIN - HOMO SAPIENS (HUMAN), 404 aa (fragment). | 2.30E-220 | |
| 195 | cg43062833 | 1567 | TGAAAAGTATTA | A | T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC: Q93088 BETAINE-- HOMOCYSTEINE S- METHYLTRANSFERASE (EC 2.1.1.5) - Homo sapiens (Human), 406 aa. | 2.10E-219 | 5 |
| 196 | cg43959148 | 342 | AGACTAGTGTG | C | gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC: O75955 FLOTILLIN-1 - HOMO SAPIENS (HUMAN), 427 aa. | 1.40E-215 | 6 |

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|-----|------------|------|---|----------|--|----------------------|------------------|--|-----------|---------------|
| 197 | cg43950766 | 385 | GTTTACACATTAG TGAAACCTGCATT TC[gap]ATGGGG GGGGGGGG TACACAGTA | C gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD4491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa. | 5.30E-214 | 22 |
| 198 | cg43958860 | 1340 | TCTGTCTTTAT TTAACAAAAAAT GT[C]ATTAACT GTAACCTGGAA TCAAG | T C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P48745 NOV PROTEIN HOMOLOG PRECURSOR (NOVH)- Homo sapiens (Human), 357 aa. | 6.00E-206 | 8 (8d24.1) |
| 199 | cg43968205 | 1516 | CTATAGCAGAG GGGGTTATGGG GGC[G/A]GGAGG GTAGACTGACAT ACAGAAAGT | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:CAB46373 HYPOTHEICAL 71.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 653 aa (fragment). | 6.90E-206 | |
| 200 | cg43950996 | 825 | ACGCCAGTCCA GAAAGAAGGTG CTG[G/A]AGCCC CTGCTCTGTCCCT CTCCATCA | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTRMBL- ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa. | 6.20E-204 | 1 |
| 201 | cg44924222 | 1787 | TAAGGGTGAGC AGCAGCAGGAG CGC[A/T]TTGAA GAAGAAAGTAGA AGGGCATGT | A T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1)- Homo sapiens (Human), 372 aa. | 2.7E-203 | |
| 202 | cg44924222 | 1834 | ATGTCAGGCAC CGTGGCAGAC TGC[A/G]GTGAC TGGTGGCATA AGGACCTT | A G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1)- Homo sapiens (Human), 372 aa. | 2.7E-203 | |
| 203 | cg44924222 | 2073 | GTACCGGAAGG CGTAGGAGGAG ACG[A/G]GTGAGG ATGAGAGTGCAC CACGTGGTG | A G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1)- Homo sapiens (Human), 372 aa. | 2.7E-203 | |

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|-----|------------|------|---|----------|--|----------------------|------------------|--|----------|---|
| 204 | cg44916575 | 1943 | GAGGACAAAAA CAGAAAGCCCT GTG[A]TGTG GGAAAACCTCG CTGCAGAGA | A T | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene SPTRMBL- ACC:Q16842 BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.4) (CMP-N- ACETYLNEURAMINATE-BETA- GALACTOSAMIDE-ALPHA-2,3- SIALYL-TRANSFERASE) - HOMO SAPIENS (HUMAN), 350 aa. | 3.7E-197 | |
| 205 | cg42650960 | 2321 | GGCTGGAGTGC AGTGGCACGAT CTC[G/A]GCTCA CTGCAAGCCTC GCCCTCCCG | G A | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene SWISSPROT- ACC:Q10981 GALACTOSIDE 2-L- FUCOSYLTRANSFERASE 2 (EC 2.4.1.69) (GDP-L-FUCOSE:BETA-D- GALACTOSIDE 2-ALPHA-L- FUCOSYLTRANSFERASE 2) (ALPHA(1,2)FT 2) (FUCOSYLTRANSFERASE 2) (SECRETOR BLOOD GROUP ALPHA-2- FUCOSYLTRANSFERASE) (SECRETOR FACTOR) (SE) (SE2)- Homo sapiens (Human), 343 aa. | 2E-189 | |
| 206 | cg43947129 | 2163 | CTGGGGCGTC CATGGTGGGGC GGC[G/C]AGGGC GGTAGTCAGC CAAGGAGGA | G C | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene SWISSPROT- ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa. | 3E-188 | |
| 207 | cg43922383 | 199 | ATCTGAAAATGG TGTGGGGCGTC GC[G/A]CGCGCC AGCTATCGTCA GTGCCCTT | G A | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene SPTRMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |
| 208 | cg43922383 | 222 | CGCGCGCAGC TATCGTCAGTGC CT[gap]GTTATT GCCATTGGGTTT GTGACTGT | gap G | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene SPTRMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |

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|-----|------------|------|---|---|-----|--|----------------------|------------------|---|-----------|----|
| 209 | cg43922383 | 239 | TCAAGTGCCTTA TTGCCATTGGGT TT[gap]GTGACT GTTGATATAGTG ACGACCT | T | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |
| 210 | cg43922383 | 250 | ATTCGCCATTGG GTTTGTGACTGT TG[A/G]TATAGT GACGGACCTCAG GAGCAACA | A | G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |
| 211 | cg43922383 | 263 | TTGTGACTGTG ATATAGTGACGA C[C/G]TCAGGAG CAAACAGGTGGG TTAAVAA | C | G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |
| 212 | cg43953935 | 458 | CTTTTAAATAA ATGACTGCGAG TG[A/G]GTAA ATTCTGAGAAAA TTACATT | A | G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD41634 LYSOSOMAL TRAFFICKING REGULATOR 2 - MUS MUSCULUS (MOUSE), 703 aa (fragment). | 2.4E-177 | 13 |
| 213 | cg43933591 | 1167 | ACATTGGAAATT TTAGCTTTTTTT T[gap]GCCTCTC TACTGTGTCACT AAATAT | T | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa. | 1.70E-176 | 8 |
| 214 | cg43949875 | 2329 | CTGAGTAGCTG GGATTACAGGC GTG[T/C]GCCAC CATGCCAGCT AATTTTTG | T | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD34394 NUCLEAR PORE COMPLEX INTERACTING PROTEIN NP1P - HOMO SAPIENS (HUMAN), 350 aa. | 6.60E-175 | |
| 215 | cg43100840 | 1131 | GGACAGGGGTG CAGCTGGCAGC CGA[G/A]AAAGG GGACCACTCG GAGGGCTGG | G | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P49752 HYPOTHETICAL PROTEIN ZAP113 - Homo sapiens (Human), 309 aa (fragment). | 3.20E-168 | |

| 216 | cg43922270 | 2077 | TGTATATGTTGA CGTAGGTTAGAT GT[G/A]TGAGC ATGCCAGG | G A | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa. | 1.30E-162 2 |
|-----|------------|------|--|----------|----------------------|------------------|---|-----------------|
| 217 | cg43993462 | 1461 | CAGAATGAGCT GGAGGGTTTC CTC[C/T]CTGCTT TACAATCCCTTA TTGAAGT | C T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment). | 5.10E-161 5 |
| 218 | cg43993462 | 384 | TAACATCTACA GAGTTGAAACAT A[A/C]CTGTCA ATTAAATATATT ATCTA | A C | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment). | 5.1E-161 5 |
| 219 | cg43993462 | 624 | TAGTCTCACCTC TTACCAAAAAAA A(A/gap)CAATGA ACTGGATTCA CCCACTCA | A gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment). | 5.1E-161 5 |
| 220 | cg43329741 | 996 | GCAGTGCAGGA GATGACAGAGT GAG[G/A]AGGGC CCAGAGCAGAA TTCTGGCCC | G A | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD39906 FH1/FH2 DOMAIN- CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa. | 6.7E-159 |
| 221 | cg42910688 | 1687 | AAACAAATTGG TTCAATGCCAC C[G/A]AGACATA TAGAATTGGAA CTGATA | G A | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P55040 GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa. | 7.7E-158 8 |
| 222 | cg43967474 | 969 | TGCTGGGGAC ATGGATGGGA GGA[G/gap]GG CACAGGGCCA GTGCAGATGAA | G gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:BAA76848 KIAA1004 PROTEIN HOMO SAPIENS (HUMAN), 496 aa (fragment). | 1.70E-152 11 |

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|-----|------------|------|--|---|-----|----------------------|------------------|--|-----------|---|
| 223 | cg43984140 | 160 | GCTGAGATCTTAC GGTCAAAAGC TA[C/T]AGAAAA GAAATCACTTTG AAAAACA | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC: AAC69899 SACM21 - MUS MUSCULUS (MOUSE), 721 aa. | 1.10E-150 | 6 |
| 224 | cg43990820 | 325 | CCGGTTAAAAGC GAAAAGTAAAAA A[C/A]AATCCAC AGTTGAGCAGTT GATGTG | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC: Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 3.30E-150 | 3 |
| 225 | cg43930377 | 682 | TCACAGCTGGA TTGAAAGAGTAT TT[G/A]GGAAAT GTGGCAATGTT GTTTATAT | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC: CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 7.80E-149 | 4 |
| 226 | cg43969800 | 503 | GCAAGACGTGT CAGGGGAACCA AGG[C/T]CAGA TCATTCCCCCT CATCTACA | C | T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC: P25686 DNAJ PROTEIN HOMOLOG 1 (HSJ-1) - Homo sapiens (Human), 351 aa. | 1.20E-145 | 2 |
| 227 | cg43973724 | 2109 | TATAAGTGTATG CAATAGAAATT G[G/T]ATTGTA ATAGAAAATT CCTTG | G | T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC: O75070 KIAA0483 PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment). | 1.30E-141 | 1 |
| 228 | cg43258867 | 112 | GGCCCAGTCCT GGGCCTCTGGG AGG[C/gap]TCAC GCTCCCTCCTC AGGCTGGGG | C | gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC: Q99773 HYPOTHETICAL 30.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 285 aa. | 2.60E-141 | |
| 229 | cg42907867 | 792 | GACGATGTGGA CGCTGGAGGG ATCT/gap]GGC GTTGGTTTCTG AAAGCCAGG | T | gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC: Q99769 HYPOTHETICAL 26.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 255 aa. | 1.10E-140 | 1 |

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|-----|------------|------|----------------|-----|----------------------|------------------|---|-----------|-----------------|
| 230 | cg43920176 | 2819 | AAAGCTGCTTG G | T | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to TREMBLNEW-ACC:AAD28325 LUMAN2 - HOMO SAPIENS (HUMAN), 272 aa. | 1.40E-140 | |
| 231 | cg43920176 | 2909 | ATTTGTCAATT C | T | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to TREMBLNEW-ACC:AAD28325 LUMAN2 - HOMO SAPIENS (HUMAN), 272 aa. | 1.40E-140 | |
| 232 | cg43950100 | 856 | CAAAATTACAA A | G | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa. | 1.70E-139 | 11 |
| 233 | cg43950100 | 952 | GGCACAGGGAG C | gap | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa. | 1.70E-139 | 11 |
| 234 | cg43950100 | 391 | ACATTGACCCCT G | A | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa. | 1.70E-139 | 11 |
| 235 | cg43950100 | 515 | CAGGTAGTGT C | T | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa. | 1.70E-139 | 11 |
| 236 | cg43132640 | 1317 | CTCTATGAACTC A | gap | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to SWISSNEW-ACC:P11226 MANNOSE-BINDING PROTEIN C PRECURSOR (MBP-C) (MBP1) (MANNAN-BINDING PROTEIN) (MANNOSE-BINDING LECTIN) - Homo sapiens (Human), 248 aa. | 4.20E-134 | 10 (10q11.2) |

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| 237 | cg44938448 | 1310 | TGAAAGTTAGAGT AGCTGCAAATCT CIT/gapTAAGTA TCAATGTAAAGA AGCAGAT | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.80E-129 | 1 |
| 238 | cg44938448 | 5111 | AATGCCACTTTCA AGATGGAAAGGG AA[A/G]TGAGAT GGAAAAACAACA AAAAAGGA | A G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.80E-129 | 1 |
| 239 | cg43949897 | 923 | AGCACTTTGGA GCTGGCCTCGC CCC[C]gapTAGG AGGAGGGTC CCTCCTGGGT | C gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60499 SYNTAXIN 10 - HOMO SAPIENS (HUMAN), 249 aa. | 1.80E-126 | 19 |
| 240 | cg42549778 | 1067 | GGGGGTGCTCC TGGAAGCCCCA AGA[G/C]CATCC AGGATTGCCTC CCAGCTGCC | G C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:ADD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa. | 3.70E-126 | |
| 241 | cg44028574 | 990 | CAGCTCCAGC TACCATGATGAG CC[C]gapTGCG GGCTTGGCAC AGTGAGTGT | C gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:ADD27724 CGI- 15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa. | 4.00E-122 | 20 |
| 242 | cg44035718 | 1088 | TCTCATCTAGTG CTGAAGTCTGA GG[G/A]CTCTGC AGCATCAGACC CACCTCTA | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA83010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment). | 2.20E-121 | 2 |

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| 243 | cg44035718 | 1172 | GAAGAGAAAGA TAGGTTTAATT ATT/CITGAAGTT TCATGGTGTAA ATATT | T C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BA0083010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment). | 2.20E-121 | 2 |
| 244 | cg43963595 | 1212 | CCCCCGCAGAC AGAGGCCGGAG GCTT[G]CTCTGG TGCAAGGATGT TTAATGGCAA | T G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa. | 8.50E-120 | 17 |
| 245 | cg43963595 | 1213 | CCCCGCAGACA GAGGCCGGAGG CTTT[G]CTGGT GCAGCGATGTT TAATGGCAA | T G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa. | 8.50E-120 | 17 |
| 246 | cg43963595 | 1402 | ATGTTACAGTAT GTACAAGACCC CT[CG]CCCTC GGGGACGGG GGGGACTCCG | C gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa. | 8.50E-120 | 17 |
| 247 | cg43992566 | 492 | AAATAGAGAAC CAGACCCCTCC CA[G/A]ATAATT AAGAACTGAGTT TTCCCTC | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O14530 PROTEIN 1-4 - Homo sapiens (Human), 226 aa. | 5.40E-118 | |
| 248 | cg43992566 | 670 | ATTTAAATCTGA AGCAGAAAAAAA A[A]GACAAATT TTACAAAGAATT ATTGAGC | A gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O14530 PROTEIN 1-4 - Homo sapiens (Human), 226 aa. | 5.40E-118 | |
| 249 | cg43067745 | 907 | TCCCTGCACGC CTTTACGTCAAG CT[G/A]TCACCA CAAGAGCCTTG AGTGTCCA | G A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.90E-118 | |

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| 250 | cg42697161 | 552 | ACGTGGTGGCTG GTAGTGTCTTGT TG[A/G]GTGTGA ATTCTCTCAT ACAAAAG | A G | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to SPTREMBL-ACC:O15262 RING FINGER PROTEIN - HOMO SAPIENS (HUMAN), 247 aa. | 1.00E-114 4 |
| 251 | cg43957889 | 1466 | GTGCCATGGCA TGATCTCGGCT CAC[C/T]GCAAC CTC GCCTCCC GGTTCAAG | C T | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 -HOMO SAPIENS (HUMAN), 227 aa. | 2.70E-111 12 |
| 252 | cg42391024 | 404 | AACTGCAGACA AATTTCCAATT CA[C/A]TTCTTTA CTTCCTCAAAGAT CTTCGA | C A | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to SWISSNEW-ACC:O43583 DRP1 PROTEIN (DRP) - Homo sapiens (Human), 243 aa. | 4.30E-109 |
| 253 | cg43976566 | 711 | CTTTAATGAAAC ACTTGGATCGT C[A/G]GTGCTGA AGTAAAAAGAA TGTGCTG | A G | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa. | 1.70E-107 4 |
| 254 | cg44001900 | 936 | GATGCTAAAAAG CTTCTGCGAAAT GT[G/A]TTCACG TTTAATGTTGGG AAATCCC | G A | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to TREMBLNEW-ACC:BAA83057 KIAA1105 PROTEIN - HOMO SAPIENS (HUMAN), 730 aa (fragment). | 1.20E-104 |
| 255 | cg43954569 | 471 | TTCAGCCCCACAT GACTCAGGGAC ACI[A/gap]CTCCC CAGGGTTGCT GGAGGCACC | A gap | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Homologous to SWISSNEW-ACC:P73560 DEATH DOMAIN CONTAINING PROTEIN CRADD (CASPASE AND RIP ADAPTATOR WITH DEATH DOMAIN) (RIP ASSOCIATED PROTEIN WITH A DEATH DOMAIN) - Homo sapiens (Human), 199 aa. | 1.40E-101 12 |
| 256 | cg43925519 | 791 | AGTGGCCCTT TCCCGCCCTGA AGA[C]GTTCA CACGAAAAGGC CGTTTGT | T C | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Similar to SPTREMBL- ACC:P78317 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 190 aa. | 4.40E-100 4 |

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| 257 | cg43145684 | 711 | TGGCAAATCTG CCAGCAGCGGT TGC[C/T]GAAAA TGCTGGTTCG GTGCCCTACT | C | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA81666 DNA POLYMERASE ETA - HOMO SAPIENS (HUMAN), 713 aa. | 2.90E-99 | |
| 258 | cg43981803 | 626 | ACCAAGCTCGGA GAGGGCACTTG AGA[G/T]GGTCT ATGAACAAATCT GTCTAAAAA | G | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16635 TAFAZZIN - Homo sapiens (Human), 292 aa. | 7.1E-97 | X |
| 259 | cg44006111 | 1906 | AGGCCTGTGATGC ACATGTGACACA GGT[A/G]CCTAC ATGCTCTGTTCT TGTCAAACA | A | G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:G1100182 T-CELL RECEPTOR BETA - HOMO SAPIENS (HUMAN), 311 aa. | 3.8E-95 | |
| 260 | cg44924968 | 1363 | TGGCCAGGGAC CTGAGCCCCGAG ACA[C/T]CCCTG CATTGATCCAA CCAGGTCA | C | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.8E-95 | 7 |
| 261 | cg44924968 | 1364 | GGCCAGGGACC TGAGCCCCGAGA CAC[C/T]CCCTGC ATTTGATCCAAC CAGGTCAAG | C | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.80E-95 | 7 |
| 262 | cg43977021 | 1080 | TTGCATCTAAAG TAATTCTTAAT G[T/A]ACAGGAG TAGATGAGGCC TGGCACCA | T | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAK1-4 mRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 263 | cg43977021 | 1087 | TAAAGTAATTCA TTAATGTACAGG A[G/A]TAGATGA GGCCTGGCACCA CATAGCA | G | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAK1-4 mRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |

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| 264 | cg43977021 | 1098 | ATTAATGTACAG GAGTAGATGAG GC[CT]GGCAC ACATAGCAGAA GGTATGG | C A G | T G A | SILENT- NONCODING SILENT- NONCODING SILENT- NONCODING | UNCLAS SIFIED UNCLAS SIFIED UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 mRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 265 | cg43977021 | 1107 | CAGGAGTAGAT GAGGCCCTGGCA CAC[A/G]TAGCA GAAGGGTAATGG TTCTATAGG | A | G | | | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 mRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 266 | cg43977021 | 1116 | ATGAGGCCTGG CACACATAGCA GAAG[G/A]TAAT GGTCTATAGGT GTATCTTC | G | A | | | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 mRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 267 | cg43977021 | 1169 | TAATGCACCTTG GGCTAGAGAAA TA[G/C]AAAAATC ACACGTAACAAA AACAAA | G | C | | | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 mRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 268 | cg4399373 | 303 | CACAGAAATTCA AACTTTTCA C[G/C]GAACTGG AGAAGGAC TCCGTCA | G | C | | | Human Gene Similar to SPTREMBL- ACC:O88994 HYPOTHETICAL 38.2 KD PROTEIN - RATTUS NORVEGICUS (RAT), 338 aa. | 1.50E-89 | 1 |
| 269 | cg43980889 | 915 | TTTGAGAGCTG CAGCAGAAGCG GCT[G/T]TATCA CAGACTGGATT AGTTATGA | G | T | | | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.5E-89 | |
| 270 | cg43980889 | 936 | GGCTGTATCAC AGACTGGATT GTT[G/A]TGTG AAAATACTGGAC TGTATTT | T | G | | | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.5E-89 | |

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| 271 | cg44030196 | 611 | TAGATTGTTCA TACTCAGCTCAC C[Agap]CCCATA AGACCATTCTC CTCTGGG | A gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD40853 SIRTUIN TYPE 5 - HOMO SAPIENS (HUMAN), 310 aa. | 7.4E-89 |
| 272 | cg40336929 | 317 | GGCAAACAAGTT ACAGCGGGGG AGAT[AGTTCCCT TCTCTCACCTGC CGGGGGG | T A | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O73884 PUTATIVE PHOSPHATASE - GALLUS GALLUS (CHICKEN), 268 aa. | 3.4E-84 |
| 273 | cg43920571 | 684 | AGAAAGACAGCG CGCAGAAATAG TGC[G/A]GAGAG AAATGACCAAGTA CTATTTAT | G A | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P34624 HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III - Caenorhabditis elegans, 548 aa. | 3.5E-82 |
| 274 | cg43958980 | 537 | TAAGATCCTCCA TCCCACCAAAAA T[G]ACCCACA ATGACTCCAAAT CTTGGT | A G | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43239 HYPOTHETICAL 41.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 383 aa (fragment). | 4.50E-82 |
| 275 | cg43320682 | 512 | CATTGGCAACG GCTGCCACTA GG[G]gap]CAC TGCCACTTGCCT GGCTCAAACCT | G gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment). | 6.60E-81 |
| 276 | cg42708544 | 845 | CCAGGGCTGGC TCTAGATTGGCT GG[G]gap]CCAG AATTTCTGGGT CAGTCTGAA | G gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa. | 2.60E-79 |
| 277 | cg43949796 | 637 | GGGAAGTAAAA TGAAGGAAGCA GAC[C/T]TCTTG CTCATCTTCCA AATGAAAT | C T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q94547 RGA AND ATU GENES, COMPLETE CDS - DROSOPHILA MELANOGASTER (FRUIT FLY), 579 aa. | 1.20E-75 |

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| 278 | cg43298234 | 843 | TAAGGCCAGAG CTTGTGTGCTG GGC[Agapi]CAGA AATCACCTGCTG CATCCTGTG | A | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 mRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.30E-75 | 7 |
| 279 | cg43926358 | 607 | CAGTGATGTGC TGGCCCTTCA GGG[AC]CACAG GCCCTTCAGC TTCACCGGA | A | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75272 R33729_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 152 aa (fragment). | 1.90E-74 | 19 |
| 280 | cg35060315 | 1328 | CCAAAACTATCTC ACCCTACCCCTC CC[CAGGATC CACTCTTTGGA ATGACAA | T | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.50E-73 | 11 |
| 281 | cg35060315 | 1540 | CTATTTTATCCA TCCATGTTCTCC C[A/gap]AATCTG TGCTTCTTTCA ACAGGTT | A | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.50E-73 | 11 |
| 282 | cg35060315 | 1542 | TTTATCCATCC ATGTTCTCCAA [A/gap]ATCTGTG CTTCTTTCAAC AGGTTAT | gap | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.5E-73 | 11 |
| 283 | cg35060315 | 1557 | GTTCCTCCAAAT CTGTGCTTCTT T[C/T]AACAGGTT ATATTTAAAC TATTT | C | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.5E-73 | 11 |
| 284 | cg35060315 | 1562 | CCCAAATCTGTG CTTCTTTCAAC A[G/C]GTTATA TTAAAACATT CATGA | G | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.5E-73 | 11 |

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| 285 | cg44126579 | 18 | TGTACAAC TGAT A TAGAG[A/gap]GT TTTTTTTCTT TTCTTTCAA | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa. | 1.1E-71 | 16 |
| 286 | cg43951096 | 719 | CCTCTCCTCCAA A GAGTTGGTCC GC[A/gap]AGAG GTGAAAAGAAC TCTCAATAGT | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2E-71 | 17 |
| 287 | cg43951096 | 884 | CACAGCCATAAT C ATAGAGAACAG AG[C/gap]TCTC CATGAACATCCA CCAGGCTG | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2E-71 | 17 |
| 288 | cg43960676 | 65 | AGCAGCCAGCT C TCATGGCTGCA AA[C/T]GCCCT CTCAGGTGAGT CAAAGGAG | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD43443 26S PROTEASOME SUBUNIT P40.5 - MUS MUSCULUS (MOUSE), 376 aa. | 5.3E-69 | |
| 289 | cg43323149 | 1101 | TCACCTCAGATGC AGTGTGGCTCC CC[C/G]CGCTCC CATACTGCAGC CTGCCCCCT | C G | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa. | 1E-68 | 1 |
| 290 | cg43969533 | 364 | AAGGGAAAGCCT T ATCCCTATTTTT TT[gap]CTCTT GC[GAAACAGA AGCCAAGT | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa. | 1.6E-67 | 7 |
| 291 | cg43969533 | 365 | AGGGAAAGCCTA T TCCTATTTTT TT[gap]CCCTTG CG[GAAACAGA GCCAAAGT | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa. | 1.6E-67 | 7 |

| | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD39515 HERMES - MUS MUSCULUS (MOUSE), 197 aa. | 2.3E-66 |
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| 292 | cg39376027 | 601 | CCGGGGAGGTG GTTCTGGTAATC TG[G]TGGGGA GCCGGGACAGG CGCCCCGA | T | | | |
| 293 | cg39376027 | 604 | GGGAGGTGGTT CTGGTAATCTG GGG[G]TGGAGC CGGGACAGGCG CCCCGAGTT | G | T | SILENT- NONCODING | UNCLAS SIFIED |
| 294 | cg43976681 | 210 | CTCTCTCTTCGC CGCCCACGCCAG AA[A/G]GGAGCT GGGGAGAAA AGCTGCTG | A | G | SILENT- NONCODING | UNCLAS SIFIED |
| 295 | cg43085556 | 131 | GTAAGGTAAAT GTGAATCAATAT GTT[C]TAGTTCT GGGCAATTATC TGCAAA | T | C | SILENT- NONCODING | UNCLAS SIFIED |
| 296 | cg43085556 | 149 | CAATATGTTAGT TCTGGGGCAATTA T[T/C]CTGCAAAT TCTGCCAGATAA TTAAA | T | C | SILENT- NONCODING | UNCLAS SIFIED |
| 297 | cg43085556 | 150 | AATATGTTAGTT CTGGGCAATTAT T[C/T]TGCAAATT CTGCCAGATAAT TAAAG | C | T | SILENT- NONCODING | UNCLAS SIFIED |
| 298 | cg43085556 | 30 | TTGGTTGTTCTCA AGCTTTCGCCT A[C/T]ATTTTGA CTAACCCCTGCTT ATTCC | C | T | SILENT- NONCODING | UNCLAS SIFIED |

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|-----|------------|------|--|-----|-----|--|----------------------|------------------|---|---------|
| 299 | cg43085556 | 45 | TTTTAGACTAAC C[C/T]GCCTATT CCTGTGAATCAA GTGGT | C | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa. | 8.8E-65 |
| 300 | cg43085556 | 65 | TAACCCCTGCCTTA TTCCCTGTGAATC A[A/C]GTGGTGA TCTTCAGCT TGGAAAT | A | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa. | 8.8E-65 |
| 301 | cg43920089 | 437 | GCATTGCTGCT TGTGCTTGATT T[G/A]TTTGCT CAATCCCTCCCT GGCAGC | G | A | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14716 DNAJ PROTEIN - HOMO SAPIENS (HUMAN), 135 aa. | 2E-63 |
| 302 | cg43950850 | 263 | AAACATGTTCCA TCAAAATTAGAA A[C/gap]AGCAGG TATCAGTAAAC TGGAGCA | C | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B)- Homo sapiens (Human), 119 aa. | 7.8E-62 |
| 303 | cg43950850 | 736 | AGAAAAACAC GACGACCACTA CCC[G/C]GGCCT AAGCGGTCAGC TTTCTCTC | G | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B)- Homo sapiens (Human), 119 aa. | 7.8E-62 |
| 304 | cg44128084 | 1012 | CATCCGGCTG ACGGCAGTCAC CGGT[C]GAGAC CGGCAGGGAA AGACCATGG | T | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.7E-59 |
| 305 | cg43976473 | 984 | GACGGCTCGCTG TCCCCGAGGGC CCG[gap]CTGC GCCGCTCGTG GGTACGAATAC | gap | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa. | 3.5E-59 |

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|-----|------------|-----|---------------|---|---|--|----------------------|------------------|--|----------|----|
| 306 | cg44924858 | 546 | GCTTCTGTCAGA | G | A | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Similar to SPTREMBL- AC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa. | 4.3E-59 | |
| 307 | cg44924858 | 558 | CGTTACTTTCAC | T | C | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Similar to SPTREMBL- AC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa. | 4.3E-59 | |
| | | | CGTGCGCTGCTG | | | | | | | | |
| | | | TTT/CACACAG | | | | | | | | |
| | | | GAAGAGTCTGT | | | | | | | | |
| | | | CTGTTCCA | | | | | | | | |
| 308 | cg44924858 | 755 | ACCCCAAGCTTG | A | G | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Similar to SPTREMBL- AC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa. | 4.30E-59 | |
| | | | CCCCGAGCAC | | | | | | | | |
| | | | ACA[A/G]AACTG | | | | | | | | |
| | | | TTTCTTGGCTT | | | | | | | | |
| | | | GACGAATA | | | | | | | | |
| 309 | cg43961591 | 222 | ACACCACTGGT | T | C | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Similar to SWISSPROT- AC:O35414 STATHMIN-LIKE PROTEIN B3 (RB3) - Rattus norvegicus (Rat), 189 aa. | 3.10E-58 | |
| | | | ACTCACACCCC | | | | | | | | |
| | | | CTC[T/C]GGCTG | | | | | | | | |
| | | | GGTTCTCTGGT | | | | | | | | |
| | | | GCGCCCTGTC | | | | | | | | |
| 310 | cg43924285 | 528 | CTGCATATGTT | A | G | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Similar to TREMBLNEW-ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 323 aa. | 4.20E-57 | 15 |
| | | | GCAGTTTCCAT | | | | | | | | |
| | | | C[AG]ACTTCITC | | | | | | | | |
| | | | ATAAACAAACAA | | | | | | | | |
| | | | ACATT | | | | | | | | |
| 311 | cg43924285 | 574 | ACATTTCTAGA | A | G | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Similar to TREMBLNEW-ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 323 aa. | 4.20E-57 | 15 |
| | | | AACCAAAATATG | | | | | | | | |
| | | | TA[G]GTGGCCC | | | | | | | | |
| | | | AAAGGGACTCTT | | | | | | | | |
| | | | AAGCAA | | | | | | | | |
| 312 | cg43958224 | 198 | GTTTGATCCTCA | G | A | | SILENT- NONCODING | UNCLAS SIFTED | Human Gene Similar to TREMBLNEW-ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment). | 2.30E-53 | 19 |
| | | | GCCAGGACGCA | | | | | | | | |
| | | | CA[G/A]GCCCTA | | | | | | | | |
| | | | CAAGATCCCAG | | | | | | | | |
| | | | CCCTCCAA | | | | | | | | |

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| 313 | cg43971060 | 502 | AACGGCTTAAA G CACAGCTCAG GG[G/g]CTTG GGTTTATCCC GAGGCCACAG | gap | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P31639 SODIUM(GLUCOSE COTRANSPORTER 2 (NA(+)/GLUCOSE COTRANSPORTER 2) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 672 aa. |
| 314 | cg44927952 | 342 | TATTTCATTG T TACTTATTATTC A[T/C]ATACTTA CTATATATT AAAAC | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34077 CGI- 82 PROTEIN - HOMO SAPIENS (HUMAN), 318 aa. |
| 315 | cg198883484 | 77 | AAACAAACAAAT C AACCAAACATAA A[C/T]CAACTAA GCTACACAGAAAT GTGAT | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15019 KIAA0301 - HOMO SAPIENS (HUMAN), 2047 aa (fragment). |
| 316 | cg42307356 | 11 | CGGCCGGGGC G G/TCCGAACGG CGCCCTCCGCC CCACCA | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15121 PUTATIVE FATTY ACID DESATURASE MLD - HOMO SAPIENS (HUMAN), 323 aa. |
| 317 | cg44005017 | 947 | TGGGAGGCCTG C GTTGCCCTCC CGG[C/T]GTGCT GGGACACTCTG GGTTCCTGC | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43363 HYPOTHETICAL 23.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 204 aa. |
| 318 | cg43329819 | 609 | TTGAGCTCTCCCT A ACAAGCTGGAG GC[A/C]AACAGT CAGTGGAGGGC GGGGGCC | C | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa. |
| 319 | cg43329819 | 612 | AGCTCTCCCTACA C AGCTGGAGGCCA AA[C/T]AGTCAG TGAGAGGGGG GGCCAGT | T | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa. |

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| 320 | cg43329819 | 625 | GCTGGAGGCAA ACAGTCAGTGA GAG[C/T]GGGG GGCCAGTCAGA CCCGACCAA | C T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa. | 1.40E-50 |
| 321 | cg44015618 | 980 | CAAGCCTCATAG CCACACACACA CAC[A/gap]CGTA CCACACACGCA CACACACACA | A gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment). | 8.7e-312 |
| 322 | cg44015618 | 1009 | ACCACACACGC ACACACACACA CAC[A/gap]CTTT GTGGCTCAAGT GCAGGGCCACA | A gap | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment). | 8.7e-312 |
| 323 | cg40361678 | 3074 | CAACACTTGG GAGGCCGAGGC AGGT[C]GGATC ACCTGAGGTCA GGAGTTCGA | T C | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P14222 PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN) - Homo sapiens (Human), 555 aa. | 9.1e-313 |
| 324 | cg40361678 | 3144 | GTGAAACCCCCG TCTCTACTAAAA AT[A/T]CAAAAAT TAGCCCCCAT GGTGGCG | A T | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P14222 PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN) - Homo sapiens (Human), 555 aa. | 9.1e-313 |
| 325 | cg40361678 | 3161 | CTAAAAATACAA AAATTAGCCGG GC[A/G]TGGTGG CGGATGCCCTGT AATCCAG | A G | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P14222 PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN) - Homo sapiens (Human), 555 aa. | 9.1e-313 |

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| 326 | cg43930957 | 1287 | AAAATAAAACTC | G | T | Val | SILENT-CODING | apoptosi | Human Gene Homologous to SPTREMBL-ID:Q62627 CLONE PAR-4 INDUCED BY EFFECTORS OF APOPTOSIS - RATTUS NORVEGICUS (RAT), 332 aa. | 1.6E-117 |
| 327 | cg43300636 | 413 | TTTGAAAGTTG T[G/T]GGTCAGC TGACCAAGTAG AGGATTTC | C | T | Val | SILENT-CODING | ATPase-associated | Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS F(O), F(1) AND CF(1)) - BOS TAURUS (BOVINE), 838 aa. | 1.7E-175 |
| 328 | cg43967912 | 749 | CATTCTCTCC AAAAATTCTCAG ATT/CCTTGTCGA CAGGACTCCATT CCAACC | T | C | Lys | SILENT-CODING | ATPase-associated | Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREVISIAE VACUOLAR H(+-)ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa. | 5.6E-108 |
| 329 | cg43967912 | 761 | AAAATTCTCAG ATTTGTGCACAG G[A/G]CTCCATT CCAACCTTCCA GATTAA | A | G | Ser | SILENT-CODING | ATPase-associated | Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREVISIAE VACUOLAR H(+-)ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa. | 5.6E-108 |
| 330 | cg43967912 | 773 | ATTTGTGCACAG GACTCCATTCCA A[C/T]CTTCCAG ATTAAGTTCTG AACTGT | C | T | Arg | SILENT-CODING | ATPase-associated | Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREVISIAE VACUOLAR H(+-)ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa. | 5.6E-108 |
| 331 | cg43132502 | 371 | AGTGGTGGCA CGCCGAGGCT GCT[G/A]TTACG GCTCATCTTCAT TGATTGC | G | A | Leu | SILENT-CODING | ATPase-associated | Human Gene Similar to SPTREMBL-ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa. | 9.40E-58 |

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| 332 | cg44924856 | 352 | ACACGCCAGCT AGCCGAATGAT GTTTGJGGGTC CTTGAGCCTCG ACATGATCT | T G Pro | SILENT-CODING | cadherin | Human Gene Similar to SWISSPROT ID:Q08345 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (TRK E) (PROTEIN-TYROSINE KINASE RTK 6) - HOMO SAPIENS (HUMAN), 913 aa. | 7.90E-77 | 6 (6q16) |
| 333 | cg439911318 | 2634 | AGCACTCCCCCT GGCTCACCCCT CTCT[C]CCTCG TGGTCCTTTTC ACCTGGTG | T C Ser | SILENT-CODING | collagen | Human Gene Similar to SWISSPROT ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa. | 1.30E-73 | 1 (1p34) |
| 334 | cg41553795 | 480 | CTGTGCACGTG GTTGTCGCTGA GAC[C/T]GACTA CCAGAGTTTCG CTGTCCTGT | T C Thr | SILENT-CODING | complement | Human Gene Homologous to SWISSPROT ID:P07360 COMPLEMENT C8 GAMMA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 202 aa. | 1.40E-104 | 9 (9q34.3) |
| 335 | cg43973728 | 286 | GCAAAATTCAAGAT GCAAAGCCGTG GC[C/T]AACGGG AAGGTTCTTCCGG AATGATC | T C Ala | SILENT-CODING | cyclin | Human Gene SWISSPROT ID:P51946 CYCLIN H (MO15-ASSOCIATED PROTEIN) (P37) (P34) - HOMO SAPIENS (HUMAN), 323 aa. | 2.60E-172 | 5 (5q13.3) |
| 336 | cg43312829 | 1413 | TCCAATCAAAGAT CAACAGGACTC CAATT[GTA]CT GAATATGAGGA CAATTGTA | C His | SILENT-CODING | dehydrogenase | Human Gene SWISSPROT ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF-UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa. | 0.00E+00 | 4 |

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| 337 | cg43312829 | 1422 | AGACAACAGGAA CTCCATGTAACT GA[AG]TATGAG GACAATTGAAAG AAATCAT | A | G | Glu | Glu | SILENT- CODING | dehydrog enase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |
| 338 | cg43312829 | 1452 | AGGACAATTGAA AGAAATCATGG GT[G]TGGAAA GAGCTATATTCT GTTAGAA | A | G | Val | Val | SILENT- CODING | dehydrog enase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |
| 339 | cg43312829 | 1473 | GGGTATGGAAA GAGCTATATTCT GTT[G]AATA TAAGGCCATCCT GCCACG | T | C | Val | Val | SILENT- CODING | dehydrog enase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |

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| 340 | cg43312829 | 1569 | ACTGGATATTGA GAGGAATGGAG CCGIAATGGACT CTAAACATAAA GGCTCTG | G A | Pro | SILENT-CODING | dehydrogenase | Human Gene SWISSPROT-ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF-UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING-FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |
| 341 | cg43312829 | 1623 | TTGAAACGGCTC AAGCCAGGCCAA GGAT/C/TGTAC ACCCATTGAGTA TCCAAAAC | T C | Asp | SILENT-CODING | dehydrogenase | Human Gene SWISSPROT-ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF-UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING-FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |
| 342 | cg43307992 | 652 | TCGAGGGCCCC AACTTTGAGTTCT C[CG/A]ACGGAG ACCCATGAGGA GCTGCTGT | C A | Ser | SILENT-CODING | dehydrogenase | Human Gene Homologous to SPTREMBL-ID:Q00217 MITOCHONDRIAL NADH DEHYDROGENASE-UBIQUINONE FE-S PROTEIN 8, 23 KDA SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN). 210 aa. | 1.70E-113 | 11 |
| 343 | cg43969759 | 965 | TGGCTGTGGGC TTCACCAAGCCTC AC[CT]ACCTCC TCCAGGGAGTT GACTTCAG | C T | Val | SILENT-CODING | dehydrogenase | Human Gene Homologous to SPTREMBL-ID:Q16797 NADP-DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN). 572 aa | 1.80E-109 | 11 |

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| | | | | | | | | | |
| 344 | cg39523614 | 318 | ATGCTGGATCA GATCCAGCTGC ACT[AT]AAGTGT CGAGCCGACGA AGATGGGG | A T | Leu | Leu | SILENT-CODING | dehydrogenase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) MYCOBACTERIUM LEPRAE, 389 aa. |
| 345 | cg39523614 | 360 | AAGATGGGAC AGTTTCGTCTTG AA[C]GGGTC AAGGCTTGGGT CACGGAGG | C T | Asn | Asn | SILENT-CODING | dehydrogenase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) MYCOBACTERIUM LEPRAE, 389 aa. |
| 346 | cg39523614 | 366 | GGGACAGTTTC GTCCTGAACGG CGT[TC]AAAGGC TTGGGTCAACGG AGGCTGGCG | C T | Val | Val | SILENT-CODING | dehydrogenase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) MYCOBACTERIUM LEPRAE, 389 aa. |
| 347 | cg39523614 | 613 | TCGAGGGCACG GTCTGAGTGT GCTT[C]TGGGT ACGCTTGACAA CTCTCGTGT | T C | Leu | Leu | SILENT-CODING | dehydrogenase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) MYCOBACTERIUM LEPRAE, 389 aa. |
| 348 | cg39523614 | 660 | GTGTCTGATTG CTGCTCAAGCA GT[G]A]GGATT GCCCAAGGAGC TTTAGACA | G A | Val | Val | SILENT-CODING | dehydrogenase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) MYCOBACTERIUM LEPRAE, 389 aa. |
| 349 | cg42717491 | 207 | AGGCCTCACACT CACTTCATGTT TT[C/G]ACAAAG TCCTGCCCTTC TTGATGG | C G | Val | Val | SILENT-CODING | dehydrogenase | Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa. |

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| 350 | cg42717491 | 252 | TGATGGGGCT TTCAGCTCAGG GAT[G/A]GCCTC GGCAATCATTT CTCCCTCAA | G | A | Ala | Ala | SILENT-CODING | dehydrogenase | Human Gene Similar to SWISSPROT-ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa. | 2.40E-52 |
| 351 | cg42717491 | 270 | CAGGGATGGCC TCGGCAATCATT TT[C/T]CCTCAA AAGGAGTGATT TGCCAA | C | T | Glu | Glu | SILENT-CODING | dehydrogenase | Human Gene Similar to SWISSPROT-ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa. | 2.40E-52 |
| 352 | cg42717491 | 288 | TCATTTCCTCCT CAAAGGGAGTG ATTTCCTTGCCTA TGCCCTAGGTCT TCTCCA | T | C | Lys | Lys | SILENT-CODING | dehydrogenase | Human Gene Similar to SWISSPROT-ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa. | 2.40E-52 |
| 353 | cg42717596 | 1535 | ATTTAGTATGCT GTGAGCTGTCTT TT[G]GTGTGAATC TGATTTAGTTTC AGTTC | T | G | Thr | Thr | SILENT-CODING | eph | Human Gene Homologous to SWISSPROT-ID:P48722 OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1) - MUS MUSCULUS (MOUSE), 838 aa. | 2.10E-115 |
| 354 | cg43319420 | 1557 | AGAAAGTCAGAA GGCCTCCCTGT GGC[A/C]CCGTT CATGGACCGAG ACAAAGTGA | A | C | Ala | Ala | SILENT-CODING | esterase | Human Gene Similar to SWISSPROT-ID:Q23917 3'-5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. Ipcis: SWISSPROT-ID:Q23917 3'-5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. | 3.30E-60 |

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| 355 | cg41029366 | 687 | AGTGGGGATCA GTGTGGGATGA CAC[T/C]GGGA CCTGGAGGACG CCCACGGTGG | T C | Thr | Thr | SILENT-CODING | glycoprotein | Human Gene SPTREMBL-ID:Q61003 T CELL SURFACE GLYCOPROTEIN CD6 - MUS MUSCULUS (MOUSE), 665 aa. | 1.00E-234 | 11 |
| 356 | cg42876034 | 860 | GCGCCGCCGC GGCAGGCC GAG[G/C]CCGGC TTGGCCCCGA GCCTGGACG | G C | Gly | Gly | SILENT-CODING | glycoprotein | Human Gene Similar to SWISSPROT- ID:Q07066 22 KD PEROXISOMAL MEMBRANE PROTEIN - RATTUS NORVEGICUS (RAT), 193 aa. | 2.60E-78 | |
| 357 | cg43976227 | 258 | CTGGTGTGATCT CTGTCCTTTAT GIGAIAACCACTA CTTGGTCACTG ACATGT | G A | Val | Val | SILENT-CODING | glycoprotein | Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 2.60E-60 | 18 |
| 358 | cg43916642 | 816 | GGCTGAAAGC ATATCTATACTAT TC[G/A]GAGAAG TCGCAAATAGAA AGGGAAAA | G A | Ser | Ser | SILENT-CODING | helicase | Human Gene Similar to SWISSPROT- ID:P25888 PUTATIVE ATP- DEPENDENT RNA HELICASE RHE. ESCHERICHIA COLI, 454 aa. | 2.90E-54 | 1 |
| 359 | cg43925670 | 2320 | AACCAGGCATCA CCTCGGAACCTT TC[T/C]CCATCA AGTCAGCAATCT GAATT | T C | Glu | Glu | SILENT-CODING | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR)- HOMO SAPIENS (HUMAN), 729 aa, lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR- HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0.00E+00 | 1 |

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|-----|------------|------|---------------|---|-----|---------------|------------|---|----------|---|
| 360 | cg43925670 | 2370 | TGGTCTACTCT A | G | Leu | SILENT-CODING | interferon | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTATIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa pcds:SPTRREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTATIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0.00E+00 | 1 |
| 361 | cg43925670 | 2389 | TTTTAAATTAA G | A | Ser | SILENT-CODING | interferon | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTATIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa pcds:SPTRREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTATIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0.00E+00 | 1 |
| 362 | cg43925670 | 2446 | AATCATGATGA T | C | Leu | SILENT-CODING | interferon | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTATIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa pcds:SPTRREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTATIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0.00E+00 | 1 |

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| | | | | | | | | | |
| 363 | cg44004587 | 1913 | TTTATGTCAT | G | A | Ile | Ile | SILENT-CODING | isomers |
| | | | TTTCATCAATAA | | | | | | Human Gene Homologous to |
| | | | GIG/A]ATACACA | | | | | | SPTREMBL-ID:Q13907 HOMOLOG |
| | | | TCTCTGCCAGG | | | | | | OF YEAST IPP ISOMERASE - HOMO |
| | | | AGTTGAA | | | | | | SAPIENS (HUMAN), 228 aa. |
| 364 | cg43257400 | 2144 | CATGTGGTAA | G | C | Gly | Gly | SILENT-CODING | kinase |
| | | | CTCCTCAAAGATG | | | | | | Human Gene SPTREMBL-ID:Q60680 |
| | | | G[G/C]GAGACGT | | | | | | CONSERVED HELIX-LOOP-HELIX |
| | | | TAGCACAAATGA | | | | | | UBQUITOUS KINASE - MUS |
| | | | TAGAACG | | | | | | MUSCULUS (MOUSE), 745 aa. |
| 365 | cg43931272 | 2072 | TGGGGTTCTT | A | G | Cys | Cys | SILENT-CODING | kinase |
| | | | TCCCAACCACAA | | | | | | Human Gene TREMBLNNEW- |
| | | | A[AG]CACTCCG | | | | | | ID:G2853031 TOUSLED-LIKE |
| | | | GTGGTAAATACC | | | | | | KINASE - MUS MUSCULUS |
| | | | AAATAAG | | | | | | (MOUSE), 717 aa. |
| 366 | cg42665067 | 748 | GGGGCTTCTAC | C | T | Ser | Ser | SILENT-CODING | kinase |
| | | | ATATCCCCCG | | | | | | Human Gene SWISSPROT- |
| | | | AAG[C/T]ACCTT | | | | | | ID:P08631 TYROSINE-PROTEIN |
| | | | CAGCACTCTGC | | | | | | KINASE HCK (EC 2.7.1.112) (P59- |
| | | | AGGAGCTGG | | | | | | HCK AND P60-HCK) (HEMOPOIETIC |
| 367 | cg43982923 | 634 | CGATGCAGAAA | A | G | Glu | Glu | SILENT-CODING | kinase |
| | | | TACGAGAAA | | | | | | CELL KINASE) - HOMO SAPIENS |
| | | | GG[A/G]AAGAT | | | | | | (HUMAN), 526 aa. |
| | | | TGGGGAGGCA | | | | | | |
| | | | CCTACGGAA | | | | | | |
| 368 | cg43982923 | 655 | TGGAAAAGATTG | C | T | Tyr | Tyr | SILENT-CODING | kinase |
| | | | GGGAAGGCACC | | | | | | Human Gene SWISSPROT- |
| | | | TA[C/T]GGAAC | | | | | | ID:P49615 CELL DIVISION PROTEIN |
| | | | GTGTTCAAGGC | | | | | | KINASE 5 (EC 2.7.1.-) (TAU |
| | | | CAAAAACC | | | | | | PROTEIN KINASE II CATALYTIC |
| | | | | | | | | | SUBUNIT) (TPKII CATALYTIC |
| | | | | | | | | | SUBUNIT) (KINASE PSSALRE) |
| | | | | | | | | | (CRK6) - MUS MUSCULUS |
| | | | | | | | | | (MOUSE), 292 aa. |
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|-----|------------|-----|--------------|---|---|-----|-----|---------------|------------------|--|-----------|----|
| 369 | cg43982923 | 697 | CCAAAAACCGG | C | T | Ile | Ile | SILENT-CODING | kinase | Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa. | 3.60E-159 | 19 |
| 370 | cg43919086 | 576 | CGCTCAGGAGG | A | G | Gly | Gly | SILENT-CODING | kinase | Human Gene TREMBLNEW-ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 6.80E-158 | 19 |
| 371 | cg25143358 | 407 | GGGGCGCTCA | G | A | Gly | Gly | SILENT-CODING | kinase | Human Gene Similar to SWISSPROT-ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa. | 2.70E-51 | |
| 372 | cg43105476 | 514 | GGTCCCGATGC | C | T | Thr | Thr | SILENT-CODING | kinase inhibitor | Human Gene Similar to SWISSPROT-ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa. | 7.80E-86 | |
| 373 | cg43105476 | 541 | TGTGCTTCACCA | C | A | Arg | Arg | SILENT-CODING | kinase inhibitor | Human Gene Similar to SWISSPROT-ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa. | 7.80E-86 | |
| 374 | cg43105476 | 595 | GCAAAGGGCAGG | C | T | Glu | Glu | SILENT-CODING | kinase inhibitor | Human Gene Similar to SWISSPROT-ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa. | 7.80E-86 | |

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|--|-----|------------|-----|--|---|-----|-----|---------------|------------------|---|---------------------|
| | 375 | cg43105476 | 616 | TATCCTCGATGT A TAACATCAGCTT G[A/G]AACTCCA GCAAAGTCTGTA AAGTGT | G | Phe | Phe | SILENT-CODING | Kinase inhibitor | Human Gene Similar to SWISSPROT-ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa. | 7.80E-86 |
| | 376 | cg43939695 | 410 | CAGGGAAACGC T AATGGGAACGC CAG[T/C]ATCAA CATCACGGACA TCTCAAAGGA | C | Ser | Ser | SILENT-CODING | Kinasereceptor | Human Gene SWISSPROT-ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 (15q25) |
| | 377 | cg43939695 | 419 | GCAATGGGAAC C GCCAGTATCAA CAT[C/T]ACGGA CATCTCAAGGAA TATCACTT | T | Ile | Ile | SILENT-CODING | Kinasereceptor | Human Gene SWISSPROT-ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 (15q25) |
| | 378 | cg43939695 | 467 | CTTCATACACA C TAGAGAACTTG CG[C/A]AGTCCT CACACGCTCAA CGCCGTGG | A | Arg | Arg | SILENT-CODING | Kinasereceptor | Human Gene SWISSPROT-ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 (15q25) |
| | 379 | cg43939695 | 473 | TACACATAGAGA T ACTGGCGCAGT CTT[G]CACACG CTCAACGCCGT GGACATGG | G | Leu | Leu | SILENT-CODING | Kinasereceptor | Human Gene SWISSPROT-ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 (15q25) |
| | 380 | cg43939695 | 479 | TAGAGAACTGG G CGCAGTCTTCA CAC[G/A]CTCAA CGCCGTGGACA TGGAGCTCT | A | Thr | Thr | SILENT-CODING | Kinasereceptor | Human Gene SWISSPROT-ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 (15q25) |

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|-----|------------|------|---|--------|-----|---------------|-----------------|---|-----------|---------------|
| 381 | cg43939695 | 485 | ACTGGCGGAGT CTTCACACGGCTC AAIC/TGCCGTG GACATGGAGCT CTACACCG | C T | Asn | SILENT-CODING | kinase receptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.12) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15 (15q25) |
| 382 | cg43939695 | 509 | ACGCCGGTGGAC ATGGAGCTCA CAC[C/G]GGACT TCAAAAGCTGAC CATCAAGA | C G | Thr | SILENT-CODING | kinase receptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.12) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15 (15q25) |
| 383 | cg43939695 | 518 | ACATGGAGCTC TACACGGGACTT CA[A/G]AAGCTG ACCATCAAGAAC TCAGGAC | A G | Gln | SILENT-CODING | kinase receptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.12) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15 (15q25) |
| 384 | cg29023997 | 183 | TGGTTCCATT TCAATCTGGATG G[G/A]ATGGAGC ACCATGTGCGC ACCTGCA | G A | Gly | SILENT-CODING | kinase receptor | Human Gene SWISSPROT- ID:P36896 SERINE/THREONINE- PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37) (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB) - HOMO SAPIENS (HUMAN), 505 aa. | 9.30E-280 | 12 |
| 385 | cg43942537 | 2040 | GTTCCTCTAGGT CCTGTAAAACTT CTTCCTTCACTTC TTCTTTAGGGC ATCAT | T C | Lys | SILENT-CODING | kinesin | KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa. Ipcls:SWISSPROT- ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa. | 0.00E+00 | 10 |
| 386 | cg43975720 | 2368 | TCCGGAAAGTGG AAGTGGTACCA GTT[C/T]ACGTCT CTGGGGACCT GCTGTGGG | C T | Phe | SILENT-CODING | kinesin | Human Gene SWISSPROT- ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa. | 0.00E+00 | 2 |

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|-----|------------|------|---|---|---|-----|---------------|---------------|---|-----------|--------------|
| 387 | cg43975720 | 2398 | CCTCTGGGGAC CTGCTGGGG CAA[C/T]GCCAT CTTCCTCAAGGA GGCCAATG | C | T | Asn | SILENT-CODING | kinesin | Human Gene SWISSPROT-ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa. | 0.00E+00 | 2 |
| 388 | cg43311943 | 44 | TCGGCCCGAT GACCCCAATGT GGC[G/C]AAGAC CAAGAACAAACCT GGCTTCT | G | C | Ala | SILENT-CODING | kinesin | Human Gene Similar to SWISSPROT-ID:Q05090 KINESIN LIGHT CHAIN (KLC) - STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN), 686 aa. | 8.80E-51 | |
| 389 | cg43311943 | 80 | ACAACCTGGCTT CCTGCTACCTG AA[A/G]CAGGGC AAGTACAGGA TGCAGAGA | A | G | Lys | SILENT-CODING | kinesin | Human Gene Similar to SWISSPROT-ID:Q05090 KINESIN LIGHT CHAIN (KLC) - STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN), 686 aa. | 8.80E-51 | |
| 390 | cg43983535 | 4764 | TCTCTGGGGCC CGCTGAGGTGA CAG[C/T]AAGTG CTTTAGCTCCTG AGTCATAT | C | T | Leu | SILENT-CODING | laminin | Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa. | 0.00E+00 | 6 (6q22) |
| 391 | cg42488873 | 304 | ATCCTTTGAAAA TCTCATATTGTT T[C/T]GAGTTTC ATTACTCCATA CAAAG | C | T | Ser | SILENT-CODING | lipase | Human Gene SWISSPROT-ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa. | 9.80E-261 | |
| 392 | cg43935885 | 3848 | GGAAAGCCCCAG CTGCAGGAGCT GCT[A/G]AAGCT GCCGCCCTCA TGC GG GTAA | A | G | Leu | SILENT-CODING | MHC | Human Gene SPTREMBL-ID:P79457 MALE-SPECIFIC HISTOCOMPATIBILITY ANTIGEN HYDB - MUS MUSCULUS (MOUSE), 1186 aa. | 7.20E-173 | |
| 393 | cg44019843 | 955 | ATGTGGAGTAC ACCTTCACAGG GAT[C/T]TACAC CTTGAGTCCCT CATCAAGA | C | T | Ile | SILENT-CODING | misc_ch annel | Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa. | 0.00E+00 | 17 (17q23.1) |

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| 394 | c944929972 | 1266 | ATGTCCTGAGG GCAGTGGAGGA ACG[G/A]GATT TCCAAACAGAAAC CATTAAT | G | A | Arg | Arg | SILENT-CODING | ngf | Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa. | 4.70E-214 | 7 |
| 395 | c944926604 | 1283 | AGTCGATGTCC AGCTTGCGGGC CAC[G/A]CGGTG TAGATTGGCCA GGTTCAGCT | G | A | Arg | Arg | SILENT-CODING | nuclease | Human Gene SWISSPROT-ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) - HOMO SAPIENS (HUMAN), 939 aa. | 0.00E+00 | 3 |
| 396 | cg38642684 | 282 | GCCAGTTAATAT TGCCTAGTAATT T[C/T]GATAATC ATTAAGGTATG TAAGT | C | T | Gln | Gln | SILENT-CODING | nuclease | Human Gene Similar to SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |
| 397 | cg38642684 | 387 | AAGGATACTTCC AAGGGAGGGAC ATT[CT]GTACTT TTTCAGGTGCAA TGATTA | T | C | Gln | Gln | SILENT-CODING | nuclease | Human Gene Similar to SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |

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| 398 | cg38642684 | 405 | AGGACATTTGTA CTTTTCAGGTC C[A/T]ATGATTAA ACCACCTTAACTG TGCA | A T | Ile | Ile | SILENT-CODING | nuclease | Human Gene Similar to SWISSNEW-POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcds:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 |
| 399 | cg38642684 | 456 | TCCATTATGACAGT AGGTATAAAC TT/C]AAAAGCA CTGGCTCCACT GGGCCTG | C | Leu | Leu | SILENT-CODING | nuclease | Human Gene Similar to SWISSNEW-POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcds:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 |
| 400 | cg43919677 | 2577 | TTGAAGTAGCTC CTGAAGCTCTA C[G/A]TCTAGTG CCAGGCCAAGTG ATTGCTC | G A | Thr | Thr | SILENT-CODING | oncogene | Human Gene SWISSPROT-ID:Q00918 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT) - RATTUS NORVEGICUS (RAT), 1712 aa. | 0.00E+00 |

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| 401 | cg44005163 | 1384 | CCTGGGGCTG ATTACATTAAC GA[T/C]GCCAA AGATTATGTAAT GCTTTAT | T G | Asp Thr | SILENT- CODING SILENT- CODING | oncogen e | Human Gene SWISSPROT- ID:P12756 SKI-RELATED ONCOGENE SNOA - HOMO SAPIENS (HUMAN), 415 aa. 5.30E-229 |
| 402 | cg44005163 | 1423 | GTAATGCTTTAT TGCGCCACGA ACT[G]TTCCCTC AAAATGGTAGC GTACTTC | T C | Pro | SILENT- CODING | oncogen e | Human Gene SWISSPROT- ID:P12756 SKI-RELATED ONCOGENE SNOA - HOMO SAPIENS (HUMAN), 415 aa. 5.30E-229 |
| 403 | cg25334466 | 546 | TCAAGGACCAAG TTCACTACCCCTC CC[C]GAGGTG AAGGACTGATG CTTGCCA | T C | Pro | SILENT- CODING | oxidase | Human Gene Homologous to SWISSPROT-ID:P25689 URICASE (EC 1.7.3.3) (URATE OXIDASE)- PAPIO HAMADRYAS (HAMADRYAS BABOON), 303 aa. 1.30E-149 |
| 404 | cg42535091 | 750 | AACTGAAATACGA ACGTTGGTGA GG[A/G]AACGG TTTGATTCTTG ACAGATC | A G | Gly | SILENT- CODING | phosphat ase | Human Gene SWISSPROT- ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (SH-PTP3) (SH- PTP2) - HOMO SAPIENS (HUMAN), 593 aa. 0.00E+00 |
| 405 | cg43302847 | 1227 | GGGGTGGTGG CCATCCAGATC CTG[C/A]GGAAAG AACCCCAAAGG CTTCTTCTT | C A | Arg | SILENT- CODING | phosphat ase | Human Gene SWISSPROT- ID:P05186 ALKALINE PHOSPHATASE, TISSUE- NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP- TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa. 3.20E-286 |
| 406 | cg39728924 | 433 | GGCAAATGGTG TTGGAAAATAAT TC[G/A]AATGTTA TTGCCATGATAA CCAGAG | G A | Ser | SILENT- CODING | phosphat ase | Human Gene Similar to TREMBLNEW-ID:D1024666 PROTEIN-TYROSINE- PHOSPHATASE (EC 3.1.3.48) - MUS MUSCULUS (MOUSE), 426 aa. 1.20E-64 |

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| 407 | cg42881873 | 1564 | ACCTGAAAGCG AGC GACTGGAA AGT[AG]AACGG CGCGGGTCATA AAGTTAGCC | A | G | Val | Val | SILENT-CODING | protease | Human Gene SWISSNEW-ID:P29122 SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-) HOMO SAPIENS (HUMAN), 969 aa. Ipcds:SWISSPROT-ID:P29122 | 0.00E+00 | 15 (15q26) |
| 408 | cg42913398 | 589 | CTGTTCCGTGG ATGAGAAGATA GTC[T]CJACATT CTGAAATATTCT GCTCTTG | T | C | Val | Val | SILENT-CODING | protease | Human Gene SWISSNEW-ID:P00199 INTEGRAL MEMBRANE SERINE PROTEASE SEPRASE - HOMO SAPIENS (HUMAN), 760 aa. | 0.00E+00 | 2 |
| 409 | cg44028327 | 793 | TTCGAATTACCT ACTCAATTGTGC A[AG]ACGAATT GTTC CAAAGAG AATTTC | A | G | Gln | Gln | SILENT-CODING | proteaseI nhb | Human Gene SWISSPROT- ID:P01042 KININogen, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) - HOMO SAPIENS (HUMAN), 644 aa. | 0.00E+00 | 3 (3q27) |
| 410 | cg439879831 | 899 | CCTCAAGGACC ACTCCC AAAGA CTT[C/T]TATGTT GATGAGAACAC AACAGTCC | C | T | Phe | Phe | SILENT-CODING | proteaseI nhb | Human Gene SWISSPROT- ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa. | 1.10E-228 | 14 |
| 411 | cg43987538 | 905 | ATCATCATAAGA GAAGAAATCATT TT[A]CCAGTAG CCCCACTACCATT GAATGA | T | A | Gly | Gly | SILENT-CODING | reductase | Human Gene SWISSPROT- ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa. | 1.10E-171 | 1 (1p31) |
| 412 | cg42717608 | 142 | CCCAACAAGGTC TATGTCCAGCAC CT[G/T]CTGAAG AGAGACAAAGA ACACCTGT | G | T | Leu | Leu | SILENT-CODING | reductase | Human Gene Similar to SWISSNEW- ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa. pcds:SWISSPROT-ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa. | 1.80E-51 | |

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| 413 | cg43927378 | 4726 | ATCTGATGGAG AACTACCAGATC GTTCIGTCAGC AACCTGCCAC TGAGCGTG | T | C | Val | Val | SILENT-CODING | struct | Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa. | 0 | 2 |
| 414 | cg43945592 | 1503 | GGGCTCGGGCA GGTACACAAA CTCT[C]GTGGC TGCAAAATCCCC AGAGGAGC | T | C | Thr | Thr | SILENT-CODING | struct | Human Gene TREMBLNEW- ID:G2961252 SUPERVILLIN - HOMO SAPIENS (HUMAN), 1788 aa. | 0 | 10 |
| 415 | cg43957486 | 1475 | CTGGGGCTCCC CGCTGCCAGTG CCCI[A/G]GCCGG CGCCGCCCTGC AGGCAAGACG | A | G | Pro | Pro | SILENT-CODING | struct | Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa. | 0.00E+00 | 20 (20p11.2) |
| 416 | cg44932934 | 815 | TGCTCGAGGAT GTCAACCGCAT GTC[G/A]CCTGG GGCCGCTGGCCA TTATCTTCG | G | A | Ser | Ser | SILENT-CODING | struct | Human Gene SPTREMBL-ID:Q63358 MYOSIN HEAVY CHAIN - RATTUS NORVEGICUS (RAT), 1980 aa. | 2.10E-179 | |
| 417 | cg43100187 | 320 | AACGCCCTAGAG GGGGAGCTGGT GGC[G/C]ACATGA GCCTGCCATCC AGAATGTGC | C | A | Ala | Ala | SILENT-CODING | struct | Human Gene SWISSPROT- ID:P02549 SPECTRIN ALPHA CHAIN ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2418 aa. | 1.80E-169 | |
| 418 | cg42930605 | 333 | GGTCCATGCAC ACCTTGTGCTC GA[G/A]CCCAGC AGGGCCTTGAG CATGGCAT | G | A | Gly | Gly | SILENT-CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 | 11 (11p15.5) |
| 419 | cg42930605 | 411 | GGGGCCGGCTTG AACTTGGCCCC CAG[A/G]TCAAA TAGCTTCTGGTT CATGTCTT | A | G | Asp | Asp | SILENT-CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 | 11 (11p15.5) |

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|-----|------------|-----|--|--------------------|-------------------|---|----------------------------|--|
| | | | | | | | | |
| 420 | cg42930605 | 435 | GATCAAATAGCT TCTGGTCATGT C/C/TCCAGCT CCTTGCTGGTCT TCTGCA | C T A Tyr | Glu Glu Tyr | SILENT-CODING SILENT-CODING SILENT-CODING | struct struct struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. |
| 421 | cg42930605 | 477 | TCTTCTGCACCC TCACCTCCATGT C/G/A/TACTTCTC CTCTTCAGGCC CATGGA | G C C Ala | Tyr Ala Ala | SILENT-CODING SILENT-CODING SILENT-CODING | struct struct struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. |
| 422 | cg42930605 | 507 | TCTCCCTCTTCAG CCGGCATCGATC TT[G/C]GCGTGC AGCTGTTGCA GAGCTCCT | C T Gln | Gln | SILENT-CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. |
| 423 | cg42930605 | 516 | CAGCCGCATCG ATCTGGCGTG CAG[C/T]GTT GCAGAGGCTCC GCACCTCAG | C T Gln | Glu | SILENT-CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. |
| 424 | cg42930605 | 528 | TCTTGGCGTGC AGCTGTTGCA GAG[G/C]TCCCTG CACTTCAGACAT GGAGCCCCG | C G | Glu His | SILENT-CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. |
| 425 | cg42930605 | 558 | GCACCTTCAGAC ATGGAGCCCCG GATA[G/T]GGCAG CGGGGGCAGT GCTCCGCCA | A | Pro | SILENT-CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. |
| 426 | cg42930605 | 564 | CAGACATGGAG CCGGGGATATG CAG[G/C]GGGG GCAGTGCTCG CCAGGTTAGT | C A | Pro | SILENT-CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. |

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|-----|------------|-----|---|--------|------------|---------------|--------|---|---------|-----------------|
| 427 | cg42930605 | 615 | TCTGCTTCTCTG CCTCACGGCGG CT[C/T]CCTCCCT TCTCCAGCTCC GTGGCCG | C T | Glu Glu | SILENT-CODING | struct | Human Gene Similar to SWISSPROT-ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 | 11 (11p15.5) |
| 428 | cg42930605 | 621 | TCTCTGCCTCAC GGCGGCTCTCC TC[C/T]TTCTCCA GCTCCGTGCC GCTATCT | C T | Lys Lys | SILENT-CODING | struct | Human Gene Similar to SWISSPROT-ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 | 11 (11p15.5) |
| 429 | cg42893961 | 51 | AATGCCAGCA GAAGGGGGGG ACC[C/A]GGGGC AAGGTGGCAGC CACCAAGCA | C A | Arg Arg | SILENT-CODING | struct | Human Gene Similar to SPTREMBL-ID:Q01449 MYOSIN REGULATORY LIGHT CHAIN, CARDIAC MUSCLE ISOFORM - HOMO SAPIENS (HUMAN), 175 aa. | 2.5E-89 | |
| 430 | cg42475816 | 282 | AATCAAGACAAA CCCAGAAATTGAAA A[G/A]AAGATTG AAGCCCCACTTTC ATGCCAA | G A | Lys Lys | SILENT-CODING | struct | Human Gene Similar to SPTREMBL-ID:Q10466 TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 26926 aa. | 7.3E-85 | 2 (2q24.3) |
| 431 | cg42522566 | 337 | TGAAGAACGTAAT AGGACCGGGAG GA[T/C]GTGAAG AATGAGGTCAA CATCATGA | T C | Asp Asp | SILENT-CODING | struct | Human Gene Similar to SWISSPROT-ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.17) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa. | 6E-55 | |

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|-----|------------|-----|---|---|-----|-----|---------------|----------------------|---|----------|----|
| 432 | cg43297806 | 953 | G | A | Val | Val | SILENT-CODING | sulfotran sterase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 883 aa | 0.00E+00 | 10 |
| 433 | cg43297806 | 962 | G | A | Arg | Arg | SILENT-CODING | sulfotran sterase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 883 aa | 0.00E+00 | 10 |

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|-----|------------|------|--|---|---|-----|-----|---------------|----------------------|---|----------|----|
| 434 | cg43297806 | 973 | CCAGGGACAAG ACAGCGGTTCT GCA[G]A[GGAGC GTAGTGCCAGA GGGGTCTGG | G | A | Leu | Leu | SILENT-CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcds:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883_aa | 0.00E+00 | 10 |
| 435 | cg43297806 | 1004 | GTA GTGCCAGA GGGGTCTGGGA GG[G]A[GGCTGA AATCACCTGATA GAAGGTAT | G | A | Ala | Ala | SILENT-CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcds:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883_aa | 0.00E+00 | 10 |

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| 436 | cg43297806 | 1016 | GGGTCTGGAG GAGGCTGAAT CAC[CT]TGATA GAAGGTATAGTT CAGAGCAA | C T | Gln | SILENT-CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa | 0.00E+00 | 10 |
| 437 | cg43297806 | 1019 | TCTGGAGGAG GCTGAAATCAC CTG[A/G]TAGAA GGTATAGTTCAAG AGCAA CTG | G Tyr | Tyr | SILENT-CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa | 0.00E+00 | 10 |

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| 438 | cg43297806 | 1028 | AGGCTGAAATC ACCTGATAGAA GGT[A/G]TAGTT CAGAGCAACTG GGTCTCCAT | A G Tyr Tyr | SILENT-CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 | 0.00E+00 | 10 |
| 439 | cg43297806 | 1043 | GATAGAAGGTATT AGTCAGAGCA AC[T/A]GGGTCT CCATGGGCTCG CTGATGCT | A Pro Pro | SILENT-CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 | 0.00E+00 | 10 |
| | | | | | | | HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883_aa | | |

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|-----|------------|-----|---|---|---|-----|---------------|----------------------|--|----------|----|
| 440 | cg43297806 | 926 | CAGAGGGTAG TAAGTCAGCCA GCGT/CJTGTTAG ATGGGTAGAATA GTAGCCAG | T | C | Gln | SILENT-CODING | sulfotran sterase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N-HSST) (N-HEPARIN SULFATE) SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.[pcis: TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa. | 0.00E+00 | 10 |
| 441 | cg39515668 | 445 | CAGCACATTCA CGGTAAGCCTC GCA[A/G]AGAGC CAGCTGGCGC CAAGATAACG | A | G | Leu | SILENT-CODING | Synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.80E-72 | |
| 442 | cg39515668 | 538 | CGATGCCGAGGA TTGTCGTCAATA CG[A/G]ATCATG CCGGCATCATT CGGCTGAG | A | G | Ile | SILENT-CODING | Synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.80E-72 | |
| 443 | cg39515668 | 580 | TCGGCTGAGCG ACCAACAGTATTG CC[A/G]GCACCG AACCGGTCAATA CTGGTCGG | A | G | Arg | SILENT-CODING | Synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.80E-72 | |

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| 444 | cg39515668 | 655 | GGCGGGAGCCA ACAAGGGCCAG CAG[G/C]GGCCC AGCAAGACCT CACAGAGT | G C A A | Ala SILENT-CODING | | synthase Human Gene Similar to SWISSNEW-ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.80E-72 |
| 445 | cg21428405 | 177 | TGACCTCGCCA ATGACAGTGGC AGC[G/A]ACACC CCAATGGGGC AGATCTCCA | G A Val | Val SILENT-CODING | | synthase Human Gene Similar to SWISSNEW-ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.20E-56 |
| 446 | cg21428405 | 273 | CCTGGACTCG CTCATGAGGAT CTCTT/CITCAGG GGCGAGGTTCG GGTCCGCCA | T C Glu | Glu SILENT-CODING | | synthase Human Gene Similar to SWISSNEW-ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.20E-56 |
| 447 | cg21428405 | 327 | GAACGGGGTCG AGCTCGACGTT CAT[G/A]CCAC GTGCCAGCAC TGGCCAGCT | G A Gly | Gly SILENT-CODING | | synthase Human Gene Similar to SWISSNEW-ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.20E-56 |
| 448 | cg38924050 | 301 | TCTCGTTGATGA GGTGTACCC TC[A/G]GGGTA CGTTCACCGAC ACGGCGA | A G Arg | SILENT-CODING | | synthase Human Gene Similar to SWISSPROT-ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa. | 2.60E-53 |
| 449 | cg38924050 | 310 | TGAGGTCTGTTA CCCTCACGGGT ACGTT/CITCAC GACACCGGGCA AAACCGAAG | T C Glu | Glu SILENT-CODING | | synthase Human Gene Similar to SWISSPROT-ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa. | 2.60E-53 |

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|-----|------------|------|--|--------|------------|------------|--------------------------------|--|-----------|
| 450 | cg38924050 | 352 | AAACCGAAGTA CCGCCGAAGTT GTG[G C]GGCAT ACGGTAAATCAT CTCTGTAA | G C | Ala C | Ala Gly | SILENT-CODING SILENT-CODING | synthase Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa. | 2.60E-53 |
| 451 | cg43925970 | 1703 | GAGCACATAAG GTGAAGGTGGT GACTT[A]CCCCAG AGAACGGACCT CTATATAGG | T A | Gly Ser | Gly Ser | tm7 SILENT-CODING | Human Gene SPTREMBL-ID:000348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa. | 0.00E+00 |
| 452 | cg41616031 | 1736 | AAGGGATGTCC CCAAACTTCCAG TC[T C]GAACGC CGCACATAGTA GTCCATCA | T C | Arg Ser | Arg Ser | tm7 SILENT-CODING | Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa. | 2.90E-214 |
| 453 | cg41616031 | 1744 | TCCCCAAACTTC CAGTCTGAACG CC[G T]CACATA GTAGTCCATCAC GAACGGC | G T | Arg Arg | Arg Arg | tm7 SILENT-CODING | Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa. | 2.90E-214 |
| 454 | cg41616031 | 1796 | GGCAGATGATC AGTAGAAAAGTCA GC[T C]ACTGCC AGGTGAACAG GAAATCC | T C | Val Val | Val Val | tm7 SILENT-CODING | Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa. | 2.90E-214 |

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|-----|------------|-----|---|---|-----|-----|---------------|-----|--|-----------|
| 455 | cg42489842 | 393 | GGCTGGTCAAC ACAGGTCTTCG AC[C/G]CTGC CAGATTGTTTG AGCAAAG | C | G | Thr | SILENT-CODING | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.30E-106 |
| 456 | cg42489842 | 402 | ACACAGGTCTTCG TGACCCCTGC CA[G/A]ATTGTTT TGAGGAAAGTT GATCAGT | A | Gln | Gln | SILENT-CODING | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.30E-106 |
| 457 | cg42489842 | 423 | GCCAGATTGTTT TGAGGAAAGTT GA[T/C]CAGTCT CTTCATACCAAC ACATGCG | T | C | Asp | SILENT-CODING | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.30E-106 |

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|-----|------------|-----|---|-------------|-------------------|---------------|-----|--|-----------|
| 458 | cg42489842 | 432 | TTTGAGCAAAG TTGATCAGTCTC TTT/CICATACCAA CACATCGCTGG ATGCTG | T C C | Leu Leu Leu | SILENT-CODING | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.30E-106 |
| 459 | cg42489842 | 456 | TTCATAACCAACA CATCGCTGGAT GCT[C]GCAAGT GAATATGCCAA TACTGCT | T C C | Ala Ala Ala | SILENT-CODING | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.30E-106 |
| 460 | cg42489842 | 471 | CGCTGGATGCT GCAAGTGAATAT GC[C]TAAATACT GCTCAGAAATAT TAGGAG | C T T | Ala Ala Ala | SILENT-CODING | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.30E-106 |
| 461 | cg42927358 | 947 | TTTTGTCTTGC CAAACATCATCC T[G/A]ACAAATG GTAGCCAAACA GAGGACAA | G A A | Leu Leu Leu | SILENT-CODING | tm7 | Human Gene Similar to SWISSPROT-ID:Q15391 PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001-HOMO SAPIENS (HUMAN), 338 aa. | 1.40E-71 |

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| 462 | cg42927358 | 544 | ATGAAATTGACA CAATTGCTTCGC C[G]AGTGCTTT ATCTCATTATAT TTGTGG | G A Pro SILENT-CODING | Pro Gly SILENT-CODING | tn7 | Human Gene Similar to SWISSPROT-ID:Q15391 PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001 - HOMO SAPIENS (HUMAN), 338 aa. | 1.40E-71 |
| 463 | cg32423505 | 1056 | CCCTCCTCCCTG GCTGAGAAAAAA GTT[G/T]CCCTT GTGCAAAAACA CTAGGTACCG | G T Gly SILENT-CODING | T Gly SILENT-CODING | tn7 | Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa. | 1.20E-55 3 (3q21) |
| 464 | cg43968711 | 2389 | TATGATTGGATGT TGGAAAGAACTAT CT[C]GTTGCATT CACATTTAACCG ATTGG | C Thr SILENT-CODING | Thr SILENT-CODING | transcript | Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa. | 2.30E-292 11 |
| 465 | cg43297259 | 800 | CTCCCTGTGTGT GTCCTTAAGTGT CT[G/A]ATGAGG TGTGACTTCTGG CTAAAGC | G A Ile SILENT-CODING | A Ile Ile SILENT-CODING | transcript | Human Gene Similar to SWISSNEW-FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcis:SWISSPROT-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 7.80E-54 |
| 466 | cg20612302 | 301 | TGGAGGGGGCC CACATGGGGCC CAC[G]GCCAT CCTCAAACCTGTC CACGGGCT | C G Thr SILENT-CODING | G Thr Thr SILENT-CODING | transcript | Human Gene Similar to SPTREMBL-ID:O08996 MYELIN TRANSCRIPTION FACTOR 1-LIKE - MUS MUSCULUS (MOUSE), 1182 aa. | 1.70E-53 |
| 467 | cg43949162 | 856 | GGGCATGTTA ACCACCTCCCTT TG[C/T]GATCAT CTGGTTTAAGA AAGGAT | C T Gln SILENT-CODING | T Gln Gln SILENT-CODING | transfere se | Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa. | 1.30E-115 6 |

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|-----|------------|------|---|--------|-----|-----|---------------|-------------|---|
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| 468 | cg43928442 | 449 | CATCCACATGG GCCACGGTGA GGG[C/A]AGCCC AAAGGCTCCGT ATCTGCAGG | C A | Leu | Leu | SILENT-CODING | transferase | Human Gene Similar to SPTREMBL- ID:O09034 GLUTAHIONE S- TRANSFERASE SUBUNIT 13 - RATTUS NORVEGICUS (RAT), 226 aa. |
| 469 | cg43976701 | 1859 | GACAGCTCATTCA GAATATCGAA GATGACC | A G | Lys | Lys | SILENT-CODING | transport | Human Gene SWISSPROT-ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG (ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa. |
| 470 | cg44005525 | 975 | CTTGACTGTTAA TATTACAATGAT A[G/A]ATTCTTGT CCGAAATGTAAC CTTTG | G A | Ile | Ile | SILENT-CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. |
| 471 | cg44005525 | 1041 | ATTCTGGTGTAA AAGTGTATCCGA G[A/G]AAGAATA CACCAACCTCAT ACACGG | A G | Phe | Phe | SILENT-CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. |
| 472 | cg44005525 | 1047 | GTGTAAAAAGTGA TATCGAGAAAAGA ATT[G/A]ACACCA CCTCATACACG GATCCTG | T G | Val | Val | SILENT-CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. |
| 473 | cg44005525 | 1065 | GAAAGAATAACAC CACCCCTCATACA CTG[A/G]ATCCCTG GAGGCCCTAGA ATGGTTG | G A | Ser | Ser | SILENT-CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. |

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|-----|------------|------|---|---------------|----------|---------------|-----------|---|-----------|
| 474 | cg44005525 | 1080 | CCTCATACACG GATCCCTGGAGG CCC[C]CAGAAAT GGT[GATCTCA TTCATAGA | T C Leu | C Leu | SILENT-CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |
| 475 | cg44005525 | 1098 | GAGGCCCTAGA ATGGTTGATCTC CA[TC]CTAGA TGT[TATCGCCCTT TGGGAC | T C Glu | Glu | SILENT-CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |
| 476 | cg44005525 | 1110 | TGGTTGATCTCC ATTCTAGATGT T[A/G]TCGCCTT GGGACCAGCAC TGCAAT | A G | Asp | SILENT-CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |
| 477 | cg44005525 | 1134 | TATGCCCTTGG GACCAGCACTG CA[A/G]TTAGGT GGAGGGTCTAA AGTGATGT | A G | Asn | SILENT-CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |
| 478 | cg44005525 | 828 | TGTGGTCATAT ACTGAGTGGCA AT[A/G]CTTCCC ACCAAAGGGTC GGCAGGAT | A G | Ser | SILENT-CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |

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|-----|------------|------|---|---|---|-----|-----|---------------|---------------|---|----------|----------------|
| 479 | cg17663981 | 225 | CCGAGAACCG GGCACAGCGAG AGC[CG]TGGTG CCAAGTGGCC AAAAGTTCA | C | G | Ala | Ala | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa. | 0.00E+00 | 10 (10p11.2 3) |
| 480 | cg17663981 | 234 | CGGGCACAGCG AGGCCCTGGTG CCA[AG]GTGGC CCAAAAGTTAC GGGGGGCA | A | G | Gln | Gln | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa. | 0.00E+00 | 10 (10p11.2 3) |
| 481 | cg42907760 | 1501 | AACTCTGAAGGC CAAAGTGTGAC TC[G/A]GACTCG GAGAGCACAGT CAGCCCCC | G | A | Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15464 SHB mRNA - HOMO SAPIENS (HUMAN), 596 aa. | 0.00E+00 | 9 (9p12) |
| 482 | cg43301812 | 3795 | CTCCATGGCTG GGATGCTCTGC TGC[G/A]CTTGG TTTTGCCCGAGT GGCAGCCT | G | A | Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa. | 0.00E+00 | 3 |
| 483 | cg43917756 | 1098 | AGACACTGAC ACTGGGGAGG TGC[A/G]GAGAC TGTGCTGGATG TGGTGGAAA | A | G | Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa. | 0.00E+00 | 1 |
| 484 | cg43918356 | 2645 | CATCTTCATCTA GAAACGCCCTC AC[G/T]GAAATG GAATTGCTGCC AGACGTGG | G | T | Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 0.00E+00 | 12 |

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|-----|------------|------|--|---|---|-----|---------------|------------------|---|----------|-----------------|
| 485 | cg43924089 | 1031 | CTGTGGCCTCTC CCACGAGACAGG GT[C/T]CACATC AAACTGGGGT GTCTCCAC | C | T | Val | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:BAA31589 KIAA0614 PROTEIN HOMO SAPIENS (HUMAN), 1630 aa (fragment). | 0.00E+00 | 12 |
| 486 | cg43926428 | 2157 | CAAACCTCATGA GATTGAAGATCT G[C/G]AGCTGCT GCTCCTTGAACA TGTCTG | C | G | Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:O14924 REGULATOR OF G- PROTEIN SIGNALING 12 (RGS12)- Homo sapiens (Human), 1447 aa. | 0.00E+00 | 4 |
| 487 | cg43950657 | 2478 | CCTCTACCCATCA GGTCAGTGTCC CC[A/G]CCACCG GGGGGCTGCTG GGACTCTT | A | G | Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa. | 0.00E+00 | 21 (21q22.1) |
| 488 | cg43955358 | 3560 | CCCGACAATTGT ATCTGGCATAAA T[C/T]CCTTCAC CAGTAGATTAG GAATGA | C | T | Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO- 1,6-GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D- GLUCOSIDASE) - Homo sapiens | 0.00E+00 | 1 (1p21) |
| 489 | cg43970200 | 1374 | CATTAGAGATCT GGGCTGCAAGG TC[C/T]CCAACAT AATCAAATAAAC GATTTC | C | T | Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa. | 0.00E+00 | 1 |
| 490 | cg43970200 | 1629 | TTAACTGTGGTA TACAGTCAGTGT ATT/CIGCAAACA TTGATTTAAAGC GGTCAT | T | C | Ala | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa. | 0.00E+00 | 1 |

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|-----|------------|------|---|---|---|-----|-----|---------------|--|
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| 491 | cg43999667 | 3688 | GTACAGCCTGG TAATGGAGAAC AA[AVG]TTTGCT GTATCGTAAAG GCAGCAA | A | G | Asn | Asn | SILENT-CODING | UNCLAS Human Gene SPTREMBL-SIFIED ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment). |
| 492 | cg44009187 | 6789 | TCAACTTGCTCC AGTAGGCCGCC GG[G/T]TCTGCA GGCAGCTGGG CTGGAAGA | C | T | Glu | Glu | SILENT-CODING | UNCLAS Human Gene SWISSPROT-ACC:P42858 HUNTINGTON (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa. |
| 493 | cg44020180 | 3172 | ATGGGTAGACT CGAGTTGGTAA AT[G/A]TCCAAA CCATAGGCCAC AACCAAAAC | G | A | Asp | Asp | SILENT-CODING | UNCLAS Human Gene SPTREMBL-SIFIED ACC:Q14700 mRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). |
| 494 | cg44020180 | 3177 | TAGACTCGAGTT TGGTAATGTCC A[A/G]ACCATAG GCCACAACCAA ACAAGTG | A | G | Leu | Leu | SILENT-CODING | UNCLAS Human Gene SPTREMBL-SIFIED ACC:Q14700 mRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). |
| 495 | cg44020180 | 3199 | CCAAACCATAG GCCACAACCAA ACAA[T]GTGGAA CTCCAGACCCG AGGGAGCTG | A | T | Thr | Thr | SILENT-CODING | UNCLAS Human Gene SPTREMBL-SIFIED ACC:Q14700 mRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). |
| 496 | cg44020180 | 3211 | CCACAACCAA CAAGTGGACTC CAG[G/G]CCCCGA GGGAGCTGTGT AGATACCTC | A | G | Gly | Gly | SILENT-CODING | UNCLAS Human Gene SPTREMBL-SIFIED ACC:Q14700 mRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). |

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| 497 | cg44020180 | 3220 | AACAAAGTGGAC TCCAGACCCGA GGG[A]C]GCTGT GTAGATACCTC GCATT CGAG | A C A A | Ala SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 | |
| 498 | cg44020180 | 3226 | TGGACTCCAGA CCCGAGGGAGC TGT[G]ATTAGATA CCTCGCATTCG AGAAA CTG | G A Tyr Tyr | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 | |
| 499 | cg44020180 | 3232 | CCAGACCCGAG GGAGCTGTGTA GAT[A/G]CCTCG CATTGAGAAC TGTC TGGT | A G Gly Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 | |
| 500 | cg44020180 | 3247 | CTGTGTAGATAC CTCGCATT CGA GAI[G]ACTGTC TGGTTATAGTG ATGAATC | A G Val Val | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 | |
| 501 | cg44020180 | 3289 | TGATGAATCGCT CTCGGTGTATCT GTT[G]ACATCTG GAGAATACGGG ATTAAGT | T G Val Val | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 | |
| 502 | cg44020180 | 3298 | GCTCTGGGTGT ATCTGTACATCT GGI[A/G]GAATAC GGGATTAAGTTC TCCTCTC | A G Ser Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 | |

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|-----|------------|------|----------------|---|---|-----|-----|---------------|---------------|---|-----------|------------------|
| 503 | cg44020180 | 3312 | TGTACATCTGGAA | A | G | Leu | Leu | SILENT-CODING | UNCLAS-SIFIED | Human Gene SPTREMBL-ACC:Q14700 mRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 504 | cg44020180 | 3319 | CTGGAGAACATC | C | T | Glu | Glu | SILENT-CODING | UNCLAS-SIFIED | Human Gene SPTREMBL-ACC:Q14700 mRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 505 | cg44928323 | 2080 | AGCAGGGCAGAT | C | T | His | His | SILENT-CODING | UNCLAS-SIFIED | Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa. | 0.00E+00 | 17 (17q11.2) |
| 506 | cg44932392 | 1281 | AGAAGTTCCCTGT | G | A | Phe | Phe | SILENT-CODING | UNCLAS-SIFIED | Human Gene TREMBLNEW-ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa. | 0.00E+00 | |
| 507 | cg43991434 | 1266 | TGTCTGGTTTG | G | C | Leu | Leu | SILENT-CODING | UNCLAS-SIFIED | Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa. | 1.70E-304 | 22 |
| 508 | cg43985955 | 1994 | GCATGATAGGA | A | T | Pro | Pro | SILENT-CODING | UNCLAS-SIFIED | Human Gene SPTREMBL-ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 | |
| 509 | cg43985955 | 2009 | GAATTCCCTCCACT | T | A | Val | Val | SILENT-CODING | UNCLAS-SIFIED | Human Gene SPTREMBL-ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 | |

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|-----|------------|------|--|---|---|-----|-----|---------------|------------------|---|-----------|
| 510 | cg43985955 | 2021 | AAATGGGAAGT GTTCTGTAAATG AC[G/A]CAACCA ACCCTTAATATAC AGCCAGC | G | A | Thr | Thr | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 |
| 511 | cg43985955 | 2060 | TATAACAGCCAG CCTGTCATGAG ACCT/G]CCAAA CCCCCTTGGCC CTGTATCAG | T | G | Pro | Pro | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 |
| 512 | cg44031765 | 2070 | ACCTCGCCGTA GTAGATGTAGC GCA[G/A]CATGG ACTCGAAGGCC TGCTGTCTG | G | A | Leu | Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa. | 4.60E-279 |
| 513 | cg43252100 | 466 | TGCAAGCCCAGA GGTCTTTTAC TC[C/A]ATGGTA CCAAATGCAACT ATTCAACC | C | A | Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:BAA83037 KIAA1085 PROTEIN HOMO SAPIENS (HUMAN), 584 aa (fragment). | 4.90E-278 |
| 514 | cg43934178 | 2445 | CGATGCCATGC TTCTCCATGAGC GT[G/A]ATGAGC TCGGCCTCCGT CAGGTAGT | G | A | Ile | Ile | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa. | 1.80E-274 |
| 515 | cg43031103 | 1696 | ACATGGCCCTC CCCTGGTTGA GGAG[G/A]ACAGC AGGGGCTGGTG TGAGGTGCA | G | A | Val | Val | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa. | 6.30E-266 |
| 516 | cg43258841 | 340 | TAAATCTTGTGT GGCCATCATCC AG[T/G]GTGTGC AACATTTCACCG TCATCTT | T | G | Thr | Thr | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 |

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|-----|------------|-----|--|---|----------|-----|-------------------|-------------------|---|-----------|
| 517 | cg43258841 | 358 | CATCCAGTGTGTG GGAACATTTCAC C[G]ATCATCTTC TACTGGTATAAT TTGAA | G | A Asp | Asp | SILENT- CODING | UNCLAS- SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 |
| 518 | cg43258841 | 370 | GGAACATTTCAC CGTCATCTCTCA CT[G]GGTATAA TTTGAAAGTGC TTATT | G | Pro | Pro | SILENT- CODING | UNCLAS- SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 |
| 519 | cg43258841 | 388 | CTTCTACTGGTA TAATT[G]AAAGT G[C]TTTTATTT TTGTCATGACT CATTG | C | T Lys | Lys | SILENT- CODING | UNCLAS- SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 |
| 520 | cg43258841 | 394 | CTGGTATAATT GAAAGTGCTTA TT[CT]TTTGTC ATGACTCATTGA CAGTA | T | C Lys | Lys | SILENT- CODING | UNCLAS- SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 |
| 521 | cg43258841 | 403 | TTT[G]AAAGTGC TTATTTTGTC C[A/G]TGACTCA TTGACAGTAGCA AAGTT | A | G His | His | SILENT- CODING | UNCLAS- SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 |
| 522 | cg43258841 | 421 | TTTGTCCATGAC TCATTGACAGTA C[G]AAAGTTT GGGGTTACTCT GACTAT | G | A Phe | Phe | SILENT- CODING | UNCLAS- SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 |
| 523 | cg43258841 | 484 | AAACTCCATCCA CAAGTCCTTGCT G[A/G]ATAATCA ATCCGCTGAGCC TCATCTC | A | G Ile | Ile | SILENT- CODING | UNCLAS- SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 |
| 524 | cg43258841 | 493 | CCACAAAGTCCCT GCTGAATAATCA AT[G]CGCTGAG CCTCATCTCTAG AAATT | T | C Arg | Arg | SILENT- CODING | UNCLAS- SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 |

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| 525 | cg43971614 | 2529 | TCACCTTCCGT GGATTCTTTCT GT/CACCGTAGA CTGCATCTGCT GGCTTTC | T C Gly Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 5.30E-253 | 5 |
| 526 | cg43971614 | 2574 | GCTTCCATTG AATCCAATCCCC CIA/GTGGACAT AAGAAGAGTTCT TTCCAT | A G Pro Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 5.30E-253 | 5 |
| 527 | cg43320405 | 916 | TGTCTTCAGGC CCTCACCATG GA/GIGGCCGG AGGGCTTCAC CTTGGGG | A G C Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:CAB46424 DKFZP434G153 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 8.20E-245 | |
| 528 | cg43922856 | 1667 | TTACTGGACCAT CTATACGAAAAAT GTT/CJTCTGAAG TTTCCACCCCTT TCCTTG | T C Glu Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |
| 529 | cg43922856 | 1718 | GAGTTCTTCTTG ACCTCTTGAG ATT/CITCCCTAGT TAATGCCCTGCA GAGGTC | T C Glu Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |
| 530 | cg43991007 | 102 | CAAGAGAACAG CAAGTGCACCA AACT/CTAGCT GAAACAGAAAAA GAGACAGC | T C Leu Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75336 LIPRIN-BETA1 - HOMO SAPIENS (HUMAN), 1005 aa. | 1.80E-236 | |
| 531 | cg43940463 | 1709 | GGCTCACCAAGC TCCAGCTGGGT GTGTT/CITCATC CACCAACCAGCG TGTACTTGA | T C Glu Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q999771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa. | 3.10E-232 | |

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| 532 | cg42676981 | 1712 | GGAAGTAGGAGG TCAGGTGGGC TGT[G/A]GGGCT CTTCAGGTCAA ACACCGGA | G | A | Pro A | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa. | 5.90E-231 | 15 |
| 533 | cg43918561 | 843 | GGAGGGAGGTC TACACCAAGCT GAA[G/A]GGCCT CTACGCCACGC ACGCCCTGCG | G | A | Lys Lys | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P04177 TYROSINE 3- MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3-HYDROXYLASE) (TH) Rattus norvegicus (Rat), 498 aa. | 2.10E-224 | 11 (11p15.5) |
| 534 | cg43999712 | 566 | ACGTACCAAATG AAATGCTCTACG G[G/C]CGAAATAG GCTACATCTATG CTCTGC | G | C | Gly Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa. | 3.30E-221 | 2 |
| 535 | cg43999712 | 569 | TACCAAATGAAA TGCTCTACGGG CG[A/C]ATAGGC TACATCTATGCT CTGCTTT | A | C | Arg Arg | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa. | 3.30E-221 | 2 |
| 536 | cg43999712 | 659 | GCCATATTAGCA AGATTTGTGAAA C[A/C]ATTTAAC CTCTGGAGAAA ACCTAT | A | C | Thr Thr | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa. | 3.30E-221 | 2 |
| 537 | cg43922139 | 1860 | ACTTGACTTCC AGACACGGGTGA GG[A/G]AGGAGG AGGCTGTCCGG ACCAAAACG | A | G | Leu Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q88473 RJS - MUS MUSCULUS (MOUSE), 4836 aa. | 2.80E-218 | |
| 538 | cg43955639 | 512 | CAGGCATGGTG ATGAGGGTGC TGG[G/T]GCCAG GGAGGTGGCAG GAGCTGGCA | G | T | Ala Ala | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment). | 2.80E-215 | |

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| 539 | cg41022625 | 1066 | GCCTGGCATT GTCATCTTCTC TC[T]CGTGCTG GGCGGGTCTT TGGCAAAG | T C C C | Ser Ala Ala Ala | SILENT-CODING SILENT-CODING SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene TREMBL NEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa. | 2.00E-207 | 11 |
| 540 | cg41022625 | 1102 | TGGTCCTTGGCA AAGGGAACACG GC[G]CTTCTGG ATCGTCTTCTCC ATCATTC | G C T T | Ile Ile Ile Ile | SILENT-CODING SILENT-CODING SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene TREMBL NEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa. | 2.00E-207 | 11 |
| 541 | cg41022625 | 1111 | GCAAAGGAAC ACGGGGTTCTG GAT[G]GTCTTC TCCATCATTCAC ATCATCG | C C T T | Arg Arg Arg Arg | SILENT-CODING SILENT-CODING SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene TREMBL NEW- ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa. | 8.80E-205 | |
| 542 | cg44002669 | 1439 | CCTTGGCCTTG CACTGGGGCA GCC[G]TCTGTC CAGTTCCTCCCT CTCCCTCT | C T C T | Lys Lys Lys Lys | SILENT-CODING SILENT-CODING SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene SPTREMBL- ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa. | 2.70E-204 | 16 |
| 543 | cg43302693 | 702 | GCCCCACCTGA GTGACAATGAT GT[A]T/CJTGAC CCCACCGGGG TCGGCTCCA | T C C C | | | | Human Gene SWISSPROT- ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa. | 3.10E-202 | |
| 544 | cg43921081 | 486 | ACTTGGAAAGAA AGTATGCAGCG CT[A]GTACCAAG CCTCTCTTTGAC AAGAGAA | A A A A | | | | Human Gene SWISSPROT- ACC:Q99733 NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4 (NUCLEOSOME ASSEMBLY PROTEIN 2) (NAP2) - Homo sapiens (Human), 375 aa. | 2.80E-189 | 17 |
| 545 | cg42181143 | 1134 | CACACCAGGGC TTCTGCCACTC GA[T]CCTAAAG AACTATGATCT TTGCCTT | T C C | Gly Gly Gly | SILENT-CODING SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene SPTREMBL- ACC:O15268 SKAP55 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa. | 2.80E-189 | |

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| 546 | cg43918701 | 1667 | TTTCCAGATGC GACAGACATCAT TTT[C]GGCATA TTCTAGAAACCA AGGGCA | T | C | Pro | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60736 KE03 PROTEIN - HOMO SAPIENS (HUMAN), 367 aa (fragment). | 1.10E-170 |
| 547 | cg43926685 | 815 | AGAATTCCCTAC TGGATCACCGC AA[C]TAAGAC ATCCACAACGAT TACCGCA | C | T | Asn | SILENT-CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa. | 2.50E-168 1 (1p36.33) |
| 548 | cg44927654 | 263 | GTGCCAGCTTC TCCATGGTGGC ATC[C]GTCA GATGCTGGGT AGGGAGGT | C | T | Thr | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAAT74865 KIAA0842 PROTEIN HOMO SAPIENS (HUMAN), 1020 aa (fragment). | 7.3E-165 |
| 549 | cg43993462 | 2019 | CCAACTCATTGA CAGTGAGGGT GC[G]ATCTCCA CTTCTGTTGGT TAATTGA | G | A | Asp | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment). | 5.1E-161 5 |
| 550 | cg44010310 | 1180 | CTATATTCTCTG ATTGTGCAAAGT A[C]TAGGACAT TATATTGACAT CTTGG | C | T | Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BA32101 BCAP - HOMO SAPIENS (HUMAN), 331 aa. | 1.3E-155 13 |
| 551 | cg43950590 | 1319 | GGTGCACCATG TACAGCTGCC AAT[C]TGAGA GAAGAATCCTC CGACGGCTT | C | T | Gln | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.9E-154 7 |
| 552 | cg43950590 | 1334 | GCTGCCAACAT TGAGAGAAAGAA TCCT[C]CCGAC GGCTTCGTTAC CATCTGTC | T | C | Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 7 |

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|-----|------------|------|---|--------|------------|-------------------|-------------------|---|-----------|----|
| 553 | cg43950590 | 1361 | CGACGGCTTCG TTACCATCCGT CT[G/A]AAGCGG ATTGCACGAC CCAGTAAT | G A | Phe A | SILENT- CODING | UNCLAS- SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 554 | cg43950590 | 1370 | CGTTACCATCCT GTCTGAAGCGG ATT[G]GCACGA GCCAGTAATT GCCATT | T G | Ala G | SILENT- CODING | UNCLAS- SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 555 | cg43950590 | 1376 | CATCCTGTCTGA AGGGGATTGCA CG[A/G]GCCAG TAATTGCCCAT TCAAATCA | A G | Ala G | SILENT- CODING | UNCLAS- SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 556 | cg43950590 | 1397 | CAAGAGCCCCAG TAATTGCCCAT TC[A/G]ATCATG GTTCCTGGTCC GAGTTGGT | A G | Ile Tyr | SILENT- CODING | UNCLAS- SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 557 | cg43950590 | 1436 | GTCCGAGTTGG TAAGACCTGAGT TC[A/G]ATATAT TAGGTCCGGAT CTTGGCA | A G | Tyr Pro | SILENT- CODING | UNCLAS- SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 558 | cg43950590 | 1445 | GGTAAGACCTG AGTTCATATA TT[A/G]GGTCG GATCTGGCAC AGGCTCAT | A G | Pro Tyr | SILENT- CODING | UNCLAS- SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 559 | cg43951092 | 1484 | GAGTGAATTCA AGAAAGAGTCAA T[A/G]TATCGAT GTTGCATGTAT TTTAT | A G | Tyr Tyr | SILENT- CODING | UNCLAS- SIFIED | Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |

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|-----|------------|------|---|---|---|-----|---------------|---------------|---|-----------|----|
| 560 | cg43951092 | 1526 | TATTTTTATCTTT AGACATGGCAG CT[CA]CTGCAT CTTCATGTGTC CAA ACT | T | C | Val | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 561 | cg43951092 | 1583 | CTGCTTCTCC TGGCTCTGCCA TC[A/G]GCTCCA ATATCAATATGA ACTCGTA | A | G | Ala | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 562 | cg43951092 | 1604 | CATCAGCTCCAA TATCAATATGAA CTT[G]CGTATTG GATTAGTGGTG AGAAGAA | T | G | Arg | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 563 | cg43951092 | 1616 | TATCAATATGAA CTCGTATTGGAT TT[G]AGTGGTG AGAAGAAATTAG CAATGT | T | G | Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 564 | cg43951092 | 1640 | TTAGTGGTGA AAGAAATTAGCA AT[G]ATCATTT CAGTTGCACGA AAAGGCA | G | A | Asp | SILENT-CODING | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 565 | cg43990820 | 1135 | CATCAGTTCCA CTTCGACACATC G[G]ATTAGTCT CACAGCCACGG CCATCCA | G | A | Tyr | SILENT-CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15024 mRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 3.30E-150 | 3 |
| 566 | cg43990820 | 724 | TCGACCCCTTT CATCCTCAAAA CT[C]CGAACCC TTGGTATCCTTG TATTGA | T | C | Arg | SILENT-CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15024 mRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 3.30E-150 | |

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| 567 | cg43986914 | 319 | TCAGGAAAGG AAGCATGACAAT TT[C/T]CCACATA ACCAAAGAAGA GAAGGGA | C T | Phe Phe | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q99598 TRANSLIN-ASSOCIATED PROTEIN X (TRANSLIN-ASSOCIATED FACTOR X) - Homo sapiens (Human), 290 aa. |
| 568 | cg43119818 | 1245 | AAGAAATTATCA ATGTGGGCAT TCIT/CITTCATG TAAAATTTGAGG ACAACG | C Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P00915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa. |
| 569 | cg44027444 | 681 | CAGTGCCAGAG TCCAGGAACTG AAC[A/G]TCAAG AGCCCCGGCTGC TGTGAACAT | G Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA76379 TUDOR REPEAT ASSOCIATOR WITH PCTAIRE 2 - HOMO SAPIENS (HUMAN), 468 aa (fragment). |
| 570 | cg29351416 | 429 | CCACACAGGAC ACTGTGGTGGC CCTT[C]GATGC TCTGTCCAATA CGGAGCAG | T C | Leu Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. |
| 571 | cg29351416 | 435 | AGGACACTGTG GTGGCCCTTG TGCTT[C]CTGTC CAAATACGGAG CAGCTACTT | T C | Ala Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. |

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| 572 | cg29351416 | 546 | AGTCCAAAGTAG ACAAACAGTAATC GIC/TCTGTTACT GCAGCAGGTCT CATTAC | C T | Arg Tyr | SILENT-CODING Tyr | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGicus (RAT). 1487 aa. |
| 573 | cg29351416 | 645 | TGTATGCTCAGA CCACGGCTGAGA TA[C/T]AACATGC CCTGGAGAAAG CAGCAGC | C T | Arg Tyr | SILENT-CODING Tyr | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGicus (RAT). 1487 aa. |
| 574 | cg29351416 | 648 | ATGCTCAGACC ACGCTGAGATA CAA[C/T]ATGCC CTTGGAGAAAG AGCAGCCTG | C T | Asn Asn | SILENT-CODING Asn | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGicus (RAT). 1487 aa. |
| 575 | cg43950273 | 530 | GGTCCTCAATAA AGTAGTTATGCC A[C/A]GTCCCTGA TCCACATAGATA GCTGAA | C A | Thr Thr | SILENT-CODING Thr | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB45700 HYPOTHETICAL 32.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 287 aa (fragment). |

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| 576 | cg44930828 | 555 | TCAACACAAGG CAGCCACAGGC CAA[AG]ATCATT GTATTGGGTTT TTACCTC | A | G | Lys | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 577 | cg44930828 | 564 | GGCAGCCACAG GCCAAAATCATT GT[A]GTTGGGT TTGTTACCTCGA GGTGAGA | A | G | Val | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 578 | cg44930828 | 591 | TGGGTTTGTAC CTCGAGGTGAG AA[AG]CCCAAT CCTTTGAGGCA AAAGAACG | A | G | Lys | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 579 | cg44930828 | 597 | TGTTACCTCGAGT GTGAGAAACCC AAT[C]CCCTTG GGCAAAAGAAC GCCAAGG | C | Asn | Asn | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |

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| 580 | cg44930828 | 603 | CTCGAGGTGAG AAACCCAATCCT TT[G/A]AGGC/A AAGAACGCCAA GGTGAACC | G | A | Leu | Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 581 | cg44930828 | 615 | AACCCCAATTCTT TGAGGCAAAAG AA[C/T]GCCAAG GTGAACCAA CTCAAGG | C | T | Asn | Asn | SILENT-CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 582 | cg44930828 | 630 | GGCAAAAGAAC GCCAAGGTGAA CCA[A/G]CTCCCT CAAGGTTTCGCT GCCGAAGC | A | G | Gln | Gln | SILENT-CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 583 | cg44930828 | 645 | AGGTGAACCAA CTCCCTCAAGGTT TC[G/C]CTGCCG AAGCTTGCCAA CGTGCAGC | G | C | Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |

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| 584 | cg44930828 | 663 | AGGTTTCGCTG CCGAGCTTC CAAC(C)GTGCA GCTCCTGGATA CCGACGGGG | C | T | Asn | Asn | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 585 | cg44930828 | 690 | TGCAGCTCCTG GATACCGACGG GGGT[C]TTTG GCACTGGACG GTGCCATCT | T | C | Gly | Gly | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 586 | cg44930828 | 693 | AGCTCCTGGAT ACCGACGGGG TTT[C]GTGAC TCGGACGGTG CATCTCCT | T | C | Phe | Phe | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 587 | cg43975478 | 691 | AAAACCTGAG AAAAGATAAAC GT[C]CTGGGA GCTGAGACTGT GCTCAATC | C | T | Val | Val | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q635555 SP120 - RATTUS NORVEGICUS (RAT), 798 aa. | 4.10E-119 |
| 588 | cg42530218 | 601 | GCATGCCAGT AATAAAGATGAA GATT[C]GGGCTA GTGGTTTAGTT TTCAACA | T | C | Asp | Asp | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa. | 2.00E-118 |

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| 589 | cg43122111 | 248 | AGTGGTGGATC CCCAGGAGGAG GAG[C/A]GAAGG CGGCAGGTGG CGGGCAGA | C A | Arg Cys | SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P043770 BCL7C PROTEIN - HOMO SAPIENS (HUMAN), 217 aa. | 5.00E-115 2.90E-110 | 12 |
| 590 | cg43986282 | 656 | CTTTGGCCCATG ACTTCCTTCGTA A[G/A]CAGGATT TGCACTAGATCT CTTCAT | A A | Cys His | SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 591 | cg43986282 | 683 | AGGATTTCGAGTG AGATCTCTTCAT C[G/A]GAATTG CCACTGTTGTG CTATCTA | G A | Asp Asp | SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 592 | cg43986282 | 704 | CATCGTGAATTG CCACTGTTGTG CT[A/G]CTAAAT TTTTCCTGCAA CCATGC | A G | Asp Leu | SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 593 | cg43986282 | 731 | CTAAAATTTCC TGCAAACCATG CA[G/C]AGAAAG CAGCAGGGTG GAAGCTCC | G C | Leu Leu | SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 594 | cg43986282 | 757 | AGAAAGCAGCAT GCGGTGGAAGC TCC[T/G]GCCAT CACACTGCACC TCTTCCTGCG | T G | Arg Arg | SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 595 | cg43986282 | 779 | TCCTGCCATCAC ACTGACCTCTT CTT[A/G]GTGGT ACACGGTCTC CCACAGG | T A | Ala Ala | SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |

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|-----|------------|-----|---|--------|--------|------------|--------------------------------|--------------------------------|--|-----------|----|
| 596 | cg43986282 | 794 | GCACCTCTTCTGC CGTGGTACACG GT[CG]CTCCA CAGGCCACA CTTGGTC | C A | T G | Arg Cys | SILENT-CODING SILENT-CODING | UNCLAS-SIFIED UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 597 | cg43986282 | 800 | CTTCTGGTGG TACACGGTCC CCCA[G]CAGGC CCCACACTGGT TCCACCTC | A | G | Cys | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 598 | cg43986282 | 809 | GGTACACGGTC CTCCCACAGGC CCC[A/G]CACTT GTTTCCACCTCC CCAGACAG | A | G | Cys | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 599 | cg43986282 | 815 | CGGTCTCCCCA CAGGCCACA CTT[G]ATTTCCA CCTCCCCAGAC AGGCATT | G | A | Asn | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 600 | cg42723058 | 651 | GTCCCCCTACCA CCACCGGTAC AGAT[C]GTGAG CCTTGAGTTGCA GCAGCTGC | T | C | Asp | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BA82158 HCR PROTEIN - HOMO SAPIENS (HUMAN), 756 aa. | 1.70E-107 | |
| 601 | cg42723058 | 673 | AGATGTTGAGCC TTGAGTTGCG CAG[C/T]GGGG GAAGAACGGAA CCGCCTGGA | C | T | Leu | SILENT-CODING | UNCLAS-SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BA82158 HCR PROTEIN - HOMO SAPIENS (HUMAN), 756 aa. | 1.70E-107 | |

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|-----|------------|------|---|---------------------------|--|------------------|--|------------------------|
| 602 | cg43981269 | 727 | AGATGGCTGGC CAGATGGGCAT GTT[C/T]AACCC CATGCCATCC CTTGGGG | C T Phe T Phe | SILENT-CODING Ser Ser | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa. | 4.50E-105 |
| 603 | cg43972159 | 1381 | TAGGTTCTCGG GCTGCTGAAC GTT[C/A]GATT GAC[T/T]CTTC TCCTTGC | C A T Lys | SILENT-CODING SILENT-CODING SILENT-CODING Lys | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa. | 2.60E-102 (12q24.1) |
| 604 | cg43972159 | 1390 | GGGCTGCTGAA CTGTTCGATT GA[C/G]TTTCTT TCTCCCTGCTGT CTGTCA | C T Lys | SILENT-CODING SILENT-CODING SILENT-CODING Lys | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa. | 2.60E-102 (12q24.1) |
| 605 | cg43972159 | 1420 | CTTCTCCCTTG TGCTGTCAAG G[A/C]ACCCACT TAATACTCCCA GGGACG | A C Val | SILENT-CODING SILENT-CODING SILENT-CODING Val | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa. | 2.60E-102 (12q24.1) |
| 606 | cg43972159 | 1426 | CCTTGCTGTCTG TCACAGGAACC CA[C/T]TTAAATA TCCTCAGGGAC GTGTCAC | C T Lys | SILENT-CODING SILENT-CODING SILENT-CODING Lys | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa. | 2.60E-102 (12q24.1) |
| 607 | cg43972159 | 1465 | GGGACGTGTCA CCCACAGTCAC CCA[C/T]TTCTC TCCCATTCCGC ACTTTCT | C T Lys | SILENT-CODING SILENT-CODING SILENT-CODING Lys | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa. | 2.60E-102 (12q24.1) |
| 608 | cg43972159 | 1522 | CGGCCATCACC TTCTTGATGTCA TC[G/T]TGGCC CGGCTACGGGT CTCGGCC | C T Lys | SILENT-CODING SILENT-CODING SILENT-CODING Lys | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa. | 2.60E-102 (12q24.1) |

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| 609 | cg44911139 | 722 | GCAAGGTTCGC | C | T | Ile | SILENT-CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14499 SPlicing FACTOR - HOMO SAPIENS (HUMAN), 530 aa. | 7.90E-101 | 14 |
| 610 | cg42539705 | 165 | AAACGGAACATATG | A | Pro | Pro | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:O75229 R31449_3 - HOMO SAPIENS (HUMAN), 813 aa. (fragment). | 1.20E-100 | |
| 611 | cg42028329 | 115 | CCAAGGAGAAC | C | T | Phe | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 612 | cg42028329 | 277 | ACTTGACAACCT | A | Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 613 | cg42028329 | 295 | ACCGGTCTCGG | G | A | Arg | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 614 | cg42028329 | 310 | GGCAGGCACGG | C | T | Tyr | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 615 | cg42028329 | 316 | GACGGTTCTTCA | C | T | His | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |

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| 616 | cg42028329 | 328 | TCCTTTACGAGC ACGGCCTCTTGC CG[C/A]ACGCC CTGGATGAGAT GCCCAACGA | C A | Arg Arg | SILENT- CODING | UNCLAS- SIFIED | Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. |
| 617 | cg42028329 | 352 | GCTAGCCCTG GATGAGATGCC CAC[G/C]ACCCCT TCCTCAGGGCA CCATCAAACA | G C | Thr Gly | SILENT- CODING | UNCLAS- SIFIED | Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. |
| 618 | cg42392719 | 540 | TCGGAGAACG GCCTCAGTGCC AAG[G/T]CCCTT ACCCCTGCAGC TGGCTCTG | G T | Gly Gly | SILENT- CODING | UNCLAS- SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa. |
| 619 | cg42392719 | 606 | TCTCCCCAAG GTGGGGTCTTC TAG[A/G]TCTGT GAGGAAGAGGT | A G | Asp Asp | SILENT- CODING | UNCLAS- SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa. |
| 620 | cg42392719 | 627 | CTAGATCTGTGA GGAAAGGGTT AC[A/G]TCTCCC ACCATGCAGCT CTCTTCAG | A G | Asp Asp | SILENT- CODING | UNCLAS- SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa. |
| 621 | cg39512856 | 597 | ACGGCTGCCG GAAGCCACGTC ATA[G/A]ACGGT TTAACCCGATG GTCCTCAA | A G | Val Val | SILENT- CODING | UNCLAS- SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. |
| 622 | cg39512856 | 615 | CGTCATAGACG GTTTACCCCGA TG[G/A]TCTTCAA CGAGATGCCAC GATGCCT | A A | Asp Asp | SILENT- CODING | UNCLAS- SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. |

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| 623 | cg39512856 | 663 | CCTCATCACTGT TGAAAACAGCC AC A/G AAGCCA GCCGGAATATC TGGCGGTG | A | G | Phe | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 |
| 624 | cg39512856 | 690 | AGCCAGCCGGAA ATATCTGGCGG TGC A/G ATATC GGTAATGTTGC AGGAGAGAC | A | Ile | Ile | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 |
| 625 | cg39512856 | 708 | GCGGTGCAATA TCGGTACTGTTT GC A/TGGCAGA CCGGTATGAGG CGGAATAT | A | T | Pro | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 |
| 626 | cg39512856 | 717 | TATCGGTACTGT TTGCAGGCAGA CC G TGTATGA GGCGGAATATA TGGCTCAC | G | T | Thr | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 |
| 627 | cg37445474 | 599 | CCCTGCAAGCT CTGATGGAAC GATC T CCCCA GATCTTGGGAA AGGAGAAT | C | T | Ile | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q63615 VACUOLAR PROTEIN SORTING HOMOLOG R-VPS33A- RATTUS NORVEGICUS (RAT), 597 aa. | 2.80E-96 |
| 628 | cg30791729 | 294 | CAGATCCAGTG GCCCTCCCCCA GCT G T GTCA ACTGTGTCAG GCTGTGGCT | G | T | Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P12346 SEROTRANSFERRIN PRECURSOR (SIDEROPHILIN) (BETA-1-METAL BINDING GLOBULIN) - Rattus norvegicus (Rat) 698 aa. | 3.20E-95 |
| 629 | cg42522690 | 454 | GTGAACAGTGT AAATCAGTTTT CA T/C TGGGAC ATGAAATCCAAG GATAAGG | T | C | His | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q35884 NEBULIN-RELATED ANCHORING PROTEIN (N-RAP)- MUS MUSCULUS (MOUSE), 1175 aa. | 3.30E-94 |

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|-----|------------|-----|---|---|---|-----|-----|---------------|---------------|---|----------|----|
| 630 | cg42522690 | 625 | CTCGAAAGTCTCTGGTGAGGA TA[T/C]ACAGAA GACTATGAGCA ACCAGGG | T | C | Tyr | Tyr | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTRMBL-ACC:O35884 NEBULIN-RELATED ANCHORING PROTEIN (N-RAP) - MUS MUSCULUS (MOUSE), 1175 aa. | 3.30E-94 | 10 |
| 631 | cg43982164 | 561 | AGGTCTACGGTTGAAGCGGTCTCT CA[T/C]GTGGAT GAGTTCTGCA GCGAATGG | T | C | His | | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTRMBL-ACC:O15194 HYA22 - HOMO SAPIENS (HUMAN), 340 aa. | 1.00E-90 | |
| 632 | cg43980889 | 755 | AAGACCATTAC AAGTAGAAAATG AT[C]GCTTAC CTGGTACCGAT AGAACAG | T | C | Asp | Asp | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTRMBL-ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 633 | cg43980889 | 770 | TAGAAAATGATGCC CTTACCTGGTA C[C/T]GATAGAA CAGAAAATGTT AATATA | C | T | Thr | Thr | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTRMBL-ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 634 | cg43980889 | 776 | ATGATGCTTACCA CTGGTACCGAT AG[G/A]CAGAA AATGTTAAATAT AGACAAG | A | G | Arg | Arg | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTRMBL-ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 635 | cg43980889 | 791 | GTACCGATAGAACAGAAAATGTT AA[AVG]TATAGA CAAGTGGACCA TTTGCCCT | A | G | Lys | | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTRMBL-ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 636 | cg43955651 | 449 | CTTCACCCACG CCTGTGTTCTG GGC[G/A]CTGAC AAAGGCCACCT TGTGGTGT | G | A | Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa. | 1.10E-87 | |

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| 637 | cg43955651 | 476 | TGACAAAGGCC ACCTTGGGGT TC[G/A]GGCTTG AGCGAATGAA GCCACACT | G | A | Pro | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa. | 1.10E-87 | 2 | | | | |
| 638 | cg42353267 | 1516 | GGCCTTCGATC CAGTCCATGAG CAA[T/C]GCCAT ATAGCGGGCG CAGAGAGCT | T | C | Ala | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to TREMBLNEW-ACC:R26660_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 291 aa (fragment). | 2.60E-86 | | | | | |
| 639 | cg37027086 | 258 | GGGTCTTCAAC TGGGACAGGAG GCT[C/T]TACCC CACCAAGCCCCA AAACGAGG | T | C | Ala | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA76824 KIAA0980 PROTEIN - HOMO SAPIENS (HUMAN), 1406 aa (fragment). | 1.20E-83 | | | | | |
| 640 | cg42688841 | 449 | TCAACATAAGGT AGAAATTCTATA A[C/T]CTCAAGA AGCCGAGCGTCA TAGTATA | C | T | Arg | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSNEW-ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | | | | | |
| 641 | cg42688841 | 454 | ATAAGGTAGAAT TTCATTAACCTC A[A/G]GAAGCGA GCGTCATAGTAT AAAGAA | A | G | Leu | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSNEW-ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | | | | | |
| 642 | cg42688841 | 461 | AGAAATTCTATA ACCTCAAGAAG CG[A/G]GGCTCA TAGTATAAAGAA GGCTTGA | A | G | Ala | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSNEW-ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | | | | | |

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| 643 | cg42688841 | 476 | TCAAGAACCGA GGTCAATGAT AA[A/G]GAAGGC TTGACGACAAC AGTCTCT | A | G | Ser | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.9.3) (EC 1.6.9.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. |
| 644 | cg43982291 | 1590 | CACTGTGACCAT TTTGTCAGCCAA GIA[C]AGCAGCG GTATATTCCCAT CCAAAT | C | Leu | Leu | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | Human Gene Similar to SPTREMBL- ACC:Q28282 C3VS PROTEIN - CANIS FAMILIARIS (DOG), 659 aa. |
| 645 | cg43982291 | 1716 | GTAAGGCTGTTT TCCCAGAGCTG TC[G/A]ACACTT GGCTGGCAT TTAGACT | G | A | Val | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | Human Gene Similar to SPTREMBL- ACC:Q28282 C3VS PROTEIN - CANIS FAMILIARIS (DOG), 659 aa. |
| 646 | cg44003673 | 320 | CATGCTGGTG CCTGGTGCCAG GTG[A/G]GTGAT GACGACCTCA CGGCCTGCA | A | G | Thr | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | Human Gene Similar to TREMBLNEW-ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa. |
| 647 | cg44003673 | 449 | CATCAGAGATGT GCAGGAAGATG TC[G/A]GGGCCG CCATCAGCTG GGTAATGA | G | A | Pro | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | Human Gene Similar to TREMBLNEW-ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa. |
| 648 | cg44003673 | 470 | TGTGGGGCCG CCATCAGCTG GGT[A/G]ATGAA GCCATGGCCCT TGACCGGC | A | G | Ile | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | Human Gene Similar to TREMBLNEW-ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa. |
| 649 | cg44936941 | 1207 | CGGGCACCTCG TCGGCGATCTG CTG[T/C]CCGGT CTCCCTGCCGA GGAAGTCGT | T | C | Gly | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa. |
| | | | | | | | | 7.00E-77 |
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| 650 | cg39523553 | 704 | GGTCTGCCCGA TCCGGGATGGC TGC[C/A]GGTGG GTGATCGACGG TAGCCGGA | C A | A Arg | Arg | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 |
| 651 | cg39523553 | 721 | ATGGCTGCCGG TGGGTGATCGA CGGT/CAGGCC GGACAATGCC CGGCCGTC | T C | Gly | Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 |
| 652 | cg39523553 | 772 | GAGGACAGCCA TGGAAAGGGCAC GGAT[C]GCCA GTGCCGGGG TGATTATGG | T C | Asp | Asp | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 |
| 653 | cg39523553 | 823 | ACGTGGTGGC AACAGGCCCTCA CGG[A/G]GTGAA GGTCAGATGG CTCTTCCG | A G | Gly | Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 |
| 654 | cg39523553 | 874 | CCTGGCCCGAG CTCGATCAGGC ATC[A/G]AGGTG CCTGGAATCCTT ACTGGATG | A G | Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 |
| 655 | cg39523553 | 886 | TCGATCAGGCA TCAAGGGTGCCT GG[A/G]TCCTT ACTCGATGACG GTTTAGTGC | A G | Glu | Glu | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 |

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| 656 | cg36728314 | 399 | GCTGCTGCTTCTTG TCCTTGTGGCAA C[G/A]ATCTTCT GGCAACGTCCT TGGAAAGA | A | Ile | Ile | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa. |
| 657 | cg41677120 | 375 | TTCAGTGCACAA ATGAGATGAATG T[G/T]AACATCC CACAGTTGGCA GACAGTT | G | T | Val | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. |
| 658 | cg44126579 | 655 | AGGAGTATTCTAT CATCCCCAATG CC[G/A]TAGCCT TCATGATTGAGG AATTTCGC | G | A | Tyr | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa. |
| 659 | cg44126579 | 712 | GAGTGGCCAG CCAATCTGCATG AC[G/A]CCAGAA GTGACCACTGTT ACTTCAT | G | A | Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa. |
| 660 | cg38925480 | 73 | AGAATCTCACCA GCCTTGTGGTG CT[G/A]CATTTG CATACAACCG CATCCAGC | G | A | Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL-ACC:O75473 ORPHAN G PROTEIN-COUPLED RECEPTOR HG38 - HOMO SAPIENS (HUMAN), 907 aa. |
| 661 | cg43323149 | 544 | GCACCAAGGGAA AGCCCTACAGA CGG[A/G]CTCAG CGTCATGCAAG GGCCCTACA | A | G | Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa. |
| 662 | cg43323149 | 559 | CTACAGACGGAA CTCAGCGTCAT GCA[A/G]GGGCC CTACAGGGAAA CAGCCAGCT | A | G | Gln | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa. |

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| 663 | cg43323149 | 664 | GAAAATACAGC CGGTTAGAAGTT CA[AT/G]GCCGAT GTCCAAAAGGA AATTTC | A | G | Gln | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | |
| 664 | cg34243633 | 263 | CCACCCACAGAG ATAATGCAGGC CAG[G/C]GAGGA GATTGCACTGG ATGTCACCA | C | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa. |
| | | | | | | | | |
| 665 | cg34243633 | 431 | CAACTGCTGTCA[G CAATGCTGGCA CC[G/A]ACATAA GAACCTGGTTTC CAGCTGG | A | Val | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. |
| | | | | | | | | |
| 666 | cg34243633 | 482 | GGAGCAGGATG GCAACCCAGTGT GCC[C/T]AAAG CCCAGAAAGC CTAGGATGT | C | T | Leu | SILENT-CODING | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. |
| | | | | | | | | |
| 667 | cg43942922 | 231 | AGCCCCACATCT CAGGCCACTAG GG[G/C/A]AGAAC AAATAGGTCTC TGTCAGA | C | A | Gly | SILENT-CODING | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. |
| | | | | | | | | |
| 668 | cg43942922 | 291 | CAGTTGTCCCC ACAGGCCCTGA GCT[C/T]CAGCC TTCACCTCCAC AGACCAAGC | C | T | Leu | SILENT-CODING | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. |
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| 669 | cg43942922 | 396 | CTGTCAAGACCG CCTGAAACAGTT GT[G]CCCACA GCCCTGAGCT CCAGCCTT | G C | Val | Val | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SPTREMBL-ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. |
| 670 | cg43955219 | 1090 | CCTGGCCAACA TGGCAAAACCC CGT[CT]TCTACT AAAAATACAAA AGCCGGG | C T | Val | Val | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSPROT-ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!! Homo sapiens (Human), 593 aa. |
| 671 | cg29142822 | 401 | CACTCACAAAAA GGGCAAGAAC GC[AG]AGGAGG GATAATGTCCTG GAAGCCA | A G | Leu | Leu | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SPTREMBL-ACC:Q07320 ZEIN-ALPHA PRECURSOR (ZSF4C4) - ZEA MAYS (MAIZE), 266 aa. |
| 672 | cg43988710 | 397 | TTGGTGAAGAG GTGTACAGCA CTC[G]TAGTG TAGACTTCAGGT CACAGTT | G T | Arg | Arg | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34051 CGI-56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa. |
| 673 | cg43988710 | 404 | AGAGGTTGTAC AGCACTCGTAG TGTA[G]GACTT CAGGTCAAGT TGACAATGT | A G | Ser | Ser | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34051 CGI-56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa. |
| 674 | cg39516123 | 1049 | GCTTGGACGG CATGGGGCTAT GGT[G]GGCTAT TCTACCCGGGA GGATCGGA | T C | Gly | Gly | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSPROT-ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. |
| 675 | cg39516123 | 452 | CAGGCAGCCTG GGACAGCCCCAG CCC[G/A]TCTGC CCAGAGAACT ACCAGAGCT | G A | Pro | Pro | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSPROT-ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. |

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| 676 | cg39516123 | 563 | TCAGCTCCTCTC CGGAAAGCCAG GC[C/T]CGAGCT CAGTTCAGTGT GGCTGGCG | C T | Ala Arg | SILENT-CODING SILENT-CODING | UNCLAS UNCLAS | Human Gene Similar to SWISSPROT-ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. Human Gene Similar to SWISSPROT-ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. |
| 677 | cg39516123 | 620 | CGGTGCCTGGG AGCCCTCAGGC GCC[G/T]CACAG AACAGTGGCA CCAACTC | C T | Arg Gly | SILENT-CODING SILENT-CODING | UNCLAS UNCLAS | 5.1E-62 5.1E-62 |
| 678 | cg42731307 | 435 | GGAAATGAGCC AAAGTTCGCATG AA[T/C]CCACGG AAGTTTACCTGG TCCTCTC | C T | Gly Phe | SILENT-CODING SILENT-CODING | UNCLAS UNCLAS | 2.6E-61 Human Gene Similar to SWISSPROT-ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. |
| 679 | cg44128084 | 440 | CCGGACAACAC CGTTGGAGTTCT TT[T/C]GCCGTC AACGAGTTGCT CTGGAAA | C T | Phe Arg | SILENT-CODING SILENT-CODING | UNCLAS UNCLAS | 1.70E-59 Human Gene Similar to SPTREMBL-ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. |
| 680 | cg44128084 | 665 | TGAGCGCTCAC GCTCTCTTGCT CG[A/G]CCGCTG GTCATGAGCCC AGCTGCTC | A G | Phe Arg | SILENT-CODING SILENT-CODING | UNCLAS UNCLAS | 1.70E-59 Human Gene Similar to SPTREMBL-ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. |
| 681 | cg44128084 | 680 | TCTTGCTCGAC CGCTGGTCATG AG[C/T]CCAGCT GCTCGAGTGGAA CCTTGACA | C T | Ser Ser | SILENT-CODING SILENT-CODING | UNCLAS UNCLAS | 1.70E-59 Human Gene Similar to SPTREMBL-ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. |
| 682 | cg44128084 | 695 | TGGTCATGAGC CCAGCTGCTCG AGT[G/A]GACCT TGACATCCAGC CAGACGGTT | G A | Val Val | SILENT-CODING SILENT-CODING | UNCLAS UNCLAS | 1.70E-59 Human Gene Similar to SPTREMBL-ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. |

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| 683 | cg44128084 | 728 | ACATCCAGCCA GACGGTTTCA ATC[A/G]GCC TCGTGGTGCG ACGGGGCC | A | G | Ser | Ser | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. |
| 684 | cg30455661 | 289 | CCACATACACAA CAGCATATACT TCTCTGGGA TTCTCAAGTGGT TTGAAG | C | T | Phe | Phe | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | | Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa. |
| 685 | cg30455661 | 347 | GATTCAACAGA AGAAATCAGGCC CTC[T]GGAGA ATGCCATAGAAA CCATGGA | C | T | Leu | Leu | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | | Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa. |
| 686 | cg30455661 | 382 | CCATAGAAACCA TGAGCTGACC AAC[T]GAGAGG ATCAGCAACTGT GTTCAAGC | C | T | Asn | Asn | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | | Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa. |
| 687 | cg43302460 | 827 | AGCTCGGGAGT ACAGGGTGA TTCT[G]GAATT GCCTGTTCTTC TTCTGA | T | G | Arg | Arg | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | | Human Gene Similar to TREMBLNEW-ACC:CAB43289 HYPOTHETICAL 12.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 116 aa (fragment). |
| 688 | cg43153425 | 101 | AAGGCCGACTT TCTGTAGGAAGT AAC[T]CGTGAC CGAGAGATCA CATGTCTG | C | T | Asn | Asn | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). |
| 689 | cg43153425 | 107 | GACTTCTGTAG GAAGTAACCGT GAC[T]CGGAG ATCAGCATGTCT GTCGGTC | C | T | Asp | Asp | SILENT-CODING | UNCLAS SIFIED |
| | | | | | | | | | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). |

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| 690 | cg43153425 | 128 | GTGACCGAGAG ATCAGCATGCT GT[C/T]GGTCTG GGAAGGTACA GTTAGACT | C T Val | Val | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 |
| 691 | cg43153425 | 140 | TCAGCATGTC TG TCGGTCTGGGA AG[G/A]TCACAG TTAGACTCCAAA GGAGGAG | A Arg | Arg | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 |
| 692 | cg43153425 | 146 | TGTCTGTCGGT CTGGGAAGGTC ACA[G/A]TTAGA CTCCAAAGGAG GAGTAGTTG | A Gln | Gln | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 |
| 693 | cg43153425 | 152 | TCGGTCTGGGA AGGTACAGTTA GA[C/T]TCCAAA GGAGGAGTAGT TGGTGGGA | C T Asp | Asp | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 |
| 694 | cg43153425 | 155 | GTCTGGGAAGG TCACAGTTAGAC TC[C/T]AAAGGA GGAGTAGTTGG TGGGACCA | C T Ser | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 |
| 695 | cg43153425 | 251 | CAAATCAGCAAC CAAACCAAAAA T[A/T]CAAATTAC TATGGTTCTAC TGAAT | A T Ile | Ile | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 |
| 696 | cg43153425 | 287 | TGGGTCTACTGC AATCTCGGGTT GA[C/T]TACATG GGCTCAAGCAT CCTCATGG | C T Asp | Asp | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 |

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| 697 | cg30384142 | 40 | CTTGGCGGGCA CCAGGGGTTAA GAC[G/A]ACCCA TATT[TAGA]CT GGCACCTC | G | A | Thr | Thr | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSPROT-ACC:P44788 SUN PROTEIN (FMU PROTEIN) - Haemophilus influenzae, 451 aa. | 5.30E-56 |
| 698 | cg44015614 | 1289 | GCTCTGGCTGG GGTGCAGTATA CTTC[TCTCAC GTATTCTTATTTC CACAACCT | C | T | Glu | Glu | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSPROT-ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 |
| 699 | cg44015614 | 1295 | GCTGGGGTGCA GTATACTTCTCC ACG[A]TATTCTA TTTCCACAACTT CTTCTG | G | A | Tyr | Tyr | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSPROT-ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 |
| 700 | cg44015614 | 1313 | TCTCCACGTATT CTATTTCCACAA CT/CCTCTTCGTA TGAGATGTTCTC CATTT | T | C | Glu | Glu | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSPROT-ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 |
| 701 | cg44015614 | 1319 | CGTATTCTATT CCACAACCTCTT CTT/CIGATGAGA TGTTCTCCATT CCATGT | T | C | Ser | Ser | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSPROT-ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 |
| 702 | cg44015614 | 1325 | CTATTTCCACAA CTTCTCTGTGATG A[G/A]ATGTTCTC CATTCCATGTG TTTGT | G | A | Ile | Ile | SILENT-CODING | UNCLAS-SIFIED | Human Gene Similar to SWISSPROT-ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 |

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| 703 | cg44015614 | 1379 | AGGGCATTGCA AGAAAACCTGGCC CTT[A/G]ATAAG GAAATCAAACTC CACATGTT | A | G | Ile | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 |
| 704 | cg42380652 | 406 | AGTCCAGGCAG GGGCCACGTC CTC[T/C]CGGT CACCCCTTCCAG GAAGGGGC | T | C | Arg | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62739 RABIN3 - RATTUS NORVEGICUS (RAT), 460 aa. | 4.20E-54 |
| 705 | cg43931038 | 425 | TCTCTCTAGAG TCCCGGGGCTC AC[A/G]GCCTT GCTGCGAAGGG CAACTTGT | A | G | Ala | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGLASTER (FRUIT FLY), 254 aa. | 6.10E-54 |
| 706 | cg43931038 | 436 | GTCGGGGCT CACAGCCTTG CTG[G]GAAGG GCAACTTGTGG GCAACCTGG | C | G | Ser | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGLASTER (FRUIT FLY), 254 aa. | 6.10E-54 |
| 707 | cg43931038 | 463 | AAGGGCAACT GTGGGCAACCT GGT[C/T]AAGGA AACCTTGACTTC TTCAAATT | C | T | Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGLASTER (FRUIT FLY), 254 aa. | 6.10E-54 |
| 708 | cg43931038 | 469 | AACTTGTGGGC AACCTGGTCAA GGAA[AC]ACCTT GACTTCTTCAA TTACAAC | A | C | Val | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGLASTER (FRUIT FLY), 254 aa. | 6.10E-54 |
| 709 | cg43931038 | 478 | GCAACCTGGTC AAGGAAACCTT GACT[C/T]CTTCA AATTACAACGCC CCACCCA | T | C | Glu | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGLASTER (FRUIT FLY), 254 aa. | 6.10E-54 |

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|-----|------------|-----|---|----------------------|---------------|------------|--------------------------------|------------------|---|----------|----|
| 710 | cg43931038 | 496 | CCTTGACTTCTT CAAATTACAAC GIC/TCCACCCA TCTTACAACAA GGGGC | C T Gly Gly | T A Gly | Gly Gly | SILENT-CODING SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGLASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 711 | cg43931038 | 562 | TCACGTAGTGG TCAATAGCACCT TT[G/A]CCTCCC CCCCATGGATG CCCAACAC | G | A | Gly | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGLASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 712 | cg43338979 | 360 | CATCATCTCC TG AAGATGCTAGC AC[G/A]GTTCTT GTTATATCCAA CTCACTC | C | T | Thr | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O45933 Y43F4B.4 - CAENORHABDITIS ELEGANS, 363 aa. | 1.40E-53 | 18 |
| 713 | cg38450437 | 104 | GAATTGGTTCTG AGGAGTTGAG GA[G/A]CTTCTT TACTGATGGACCA GAAATC | G | A | Glu | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43168 KIAA0443 - HOMO SAPIENS (HUMAN), 1395 aa. | 3.50E-52 | |
| 714 | cg38450437 | 47 | CCAGGGAAAGT GCACAGCCAGA GAAT[C]TGGTC TTGCAACTGCAT CCAGTGTG | T | C | Asn | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43168 KIAA0443 - HOMO SAPIENS (HUMAN), 1395 aa. | 3.50E-52 | |
| 715 | cg43314946 | 458 | CCTTCCGGATG ACTTTCTCCGCA TC[C/T]GCC AGCAAGCTGGAC AGCATACA | C | T | Leu | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:AAD37447 BAW - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 402 aa. | 1.60E-51 | 17 |
| 716 | cg44010070 | 320 | TCAAAGCACTCG GACGGGACGG CACIT[C]TGGCG CAAGCTCTATGA CAAGAGCG | T | C | Thr | SILENT-CODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- RUBRIPES ACC:O35775 SYNCOLLIN (SIP9) - Rattus norvegicus (Rat), 145 aa. | 6.40E-51 | |

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| 717 | cg39380052 | 563 | ACCTCATCACCC CGTACCATCAG AC[C/T]CTCGAC AAGGTCACTGA GGTTTTC | C T | Thr | Thr | SILENT-CODING | UNCLAS-SIFIED |
| | | | | | | | | Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa. |
| 718 | cg39380052 | 641 | GTCGGGGCATCT GGGCCGACCTA CTCT[C/G]ACAA GATCAAATCGGAT GGTATTTC | C C | Ser | Ser | SILENT-CODING | UNCLAS-SIFIED |
| | | | | | | | | Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa. |
| 719 | cg39380052 | 662 | ACTCTGACAAGAT TCAATCGGATG GGT[C]ATTCCGC GTCCAGGATCTT TTCGACG | C T | Gly | Gly | SILENT-CODING | UNCLAS-SIFIED |
| | | | | | | | | Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa. |
| 720 | cg43329819 | 585 | TCATGACAACCT AGAACCTCCCT T[T/C]GAGCTCT CCTACAAGCTG GAGGCAA | C T | Phe | Phe | SILENT-CODING | UNCLAS-SIFIED |
| | | | | | | | | Human Gene Similar to SPTREMBL-ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa. |
| 721 | cg433298242 | 138 | CTGAAGATCTGT TGGCAGGGCTC AC[G]GAGACG GGGGTGAGGGG AGAGATCG | A G | Ser | Ser | SILENT-CODING | water_ch annel |
| | | | | | | | | Human Gene SWISSPROT-ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP)- HOMO SAPIENS (HUMAN), 342 aa. |
| 722 | cg433298242 | 150 | TGGCAGGGCTC ACAGAGACGGG GGT[G/A]AGGGG AGAGATCGTG GTTCATGAG | G A | Leu | Leu | SILENT-CODING | water_ch annel |
| | | | | | | | | Human Gene SWISSPROT-ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP)- HOMO SAPIENS (HUMAN), 342 aa. |

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|-----|------------|------|--|---|---|-----|---------------|------------------|----------------------|---|-----------|---------------|
| 723 | cg43970780 | 1501 | GGAGTTCTGGT TCTGGTAGATG GAA[G/A]CTTTCT CTTCAACAGGT CCAGACA | G | A | Ala | Val (1096) | CONSERVATI VE | apoptosi s | Human Gene SWISSNEW-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa. pcls:SWISSPROT-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa. | 2.30E-212 | 11 |
| 724 | cg43957906 | 460 | GGAGGCCCTGG CGCGTCATAT GGG[C]GCTCC TTGGGGGGAT CTCCAGGC | T | C | His | Arg (1097) | CONSERVATI VE | ATPase associated | Human Gene Similar to SWISSPROT- ID:Q16864 VACUOLAR ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (V-ATPASE F SUBUNIT) (V- ATPASE 14 KD SUBUNIT) - HOMO SAPIENS (HUMAN), 119 aa. | 2.20E-58 | 12 |
| 725 | cg43952088 | 2923 | TGAGGGGAGCC TGGCCGGCCGC GG[G/A]CAGAT GCCGGGGGGC CGCTCGCAG | G | A | Ala | Val (1098) | CONSERVATI VE | cadherin | Human Gene SPTREMBL-ID:Q150655 OB-CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa. | 0.00E+00 | 16 |
| 726 | cg43956666 | 613 | ACTCTGTCTGA GGGACAGTTTG GT[A]GTTAAAAC ACTTAAATATAG ATCCGG | A | G | Ile | Val (1099) | CONSERVATI VE | cadherin | Human Gene SWISSNEW-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP)(MER6) - HOMO SAPIENS (HUMAN), 323 aa. pcls:SWISSPROT-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP)(MER6) - HOMO SAPIENS (HUMAN), 323 aa. | 1.20E-167 | 3 (3q13.1) |

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| 727 | cg43942011 | 1327 | TCCCCATGTGA AACATCTGGCTT G[C/T]GACAGGT GATTTTTCACA GGTAGG | C T Arg His (1100) | CONSERVATI VE | complement entrecept | Human Gene Similar to TREMBLNEW-ID:E246058 COMPLEMENT RECEPTOR 2 - MUS CULUS (MOUSE), 651 aa (fragment). | 1.10E-69 | 1 (1q32) |
| 728 | cg43973728 | 987 | TATGAACCAACCCT AGATCTGAAGAA G[T/C]TGCTGTT CTGAAACAGAA GTTGGAG | C Val Ala (1101) | CONSERVATI VE | cyclin | Human Gene SWISSPROT- ID:P51946 CYCLIN H (MO15- ASSOCIATED PROTEIN) (P37) (P34) - HOMO SAPIENS (HUMAN), 323 aa. | 2.60E-172 | 5 (5q13.3) |
| 729 | cg44017721 | 291 | TCCTGCTCCTCC GTGGCCTCCTT G[G/ACAGGGCT GCCAAGCCCC GGGTCAAG | A Ala Val (1102) | CONSERVATI VE | cytochro me | Human Gene Similar to SPTRMBL- ID:O00761 CYTOCHROME OXIDASE SUBUNIT VIA HEART ISOFORM PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)) - HOMO SAPIENS (HUMAN), 97 aa. | 2.40E-52 | 22 |
| 730 | cg43273880 | 5428 | CAAAAGAAGAAA GACGACGTGAC TG[G/C]GGGTAA GAAACCATTTCG TCCAGAG | C Gly Ala (1103) | CONSERVATI VE | dna_rna _bind | Human Gene SWISSPROT- ID:O14647 CHROMODOMAIN- HELCASE-DNA-BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa. | 0.00E+00 | 15 |
| 731 | cg43992911 | 485 | GAAGAAGAACTTA TTTAAACTGAA C[A/G]ATAAAAG TGAAAAAGATAA GAAGGA | G Asn Asp (1104) | CONSERVATI VE | glycoprot ein | Human Gene SWISSPROT- ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P- GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa. | 0.00E+00 | 7 |
| 732 | cg41029366 | 890 | TGCGCCACAA AGAGGACGGCGG GCG[T/C]GGTGT GCTCAGAGCAC CAGTCCCTGG | T C Val Ala (1105) | CONSERVATI VE | glycoprot ein | Human Gene SPTRMBL-ID:Q61003 T CELL SURFACE GLYCOPROTEIN CD6 - MUS MUSCULUS (MOUSE), 665 aa. | 1.00E-234 | 11 |

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| 733 | cg43931167 | 2546 | CGAGAACTGAA GAAAGCAAGAA CAGT/G]CCTAC AAATGGATGAAC TCAAATGT | T | G | Val (1106) | Gly (1106) | CONSERVATI VE | helicase | Human Gene SWISSPROT- ID:O14232 PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 1117 aa. | 3.30E-307 | 5 |
| 734 | cg43925670 | 2360 | AATCTGAATT GTCATACTCTTC [C/T]TCATTTT AAATTAAGTTT AAATC | C | T | Arg (1107) | Lys (1107) | CONSERVATI VE | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0.00E+00 | 1 |
| 735 | cg43925670 | 2474 | TAGAACATGTT CTTGATTTTT [C/G]CCATCTTA CAGACATAAGT GAGCC | C | G | Gly (1108) | Ala (1108) | CONSERVATI VE | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0.00E+00 | 1 |

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| 736 | cg43928549 | 4637 | AATTGGCACATC | C | T | Asp | Asn (1109) | CONSERVATI VE | kinase | Human Gene SWISSNEW-ID:O00329 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, DELTA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT DELTA) (PTDINS-3-KINASE P110) (PI3K) (P110DELTA) - HOMO SAPIENS (HUMAN), 1044 aa.Ipcis:SWISSPROT-ID:Q000329 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, DELTA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT DELTA) (PTDINS-3-KINASE P110) (PI3K) (P110DELTA) - HOMO SAPIENS (HUMAN), 1044 aa.Ipcis:SPTREMBL- ID:O000329 PHOSPHOINOSITIDE 3- KINASE - HOMO SAPIENS (HUMAN), 1044 aa. | 0.00E+00 |
| 737 | cg42703622 | 409 | GAAGAAGGAAT | A | G | Ile | Val (1110) | CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa. | 3.00E-187 |
| 738 | cg44131752 | 925 | CTCTGCGTGC | C | G | Leu | Val (1111) | CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa. | 7.80E-173 |
| 739 | cg25143358 | 394 | CAGGTGGCCAT | G | T | Leu | Ile (1112) | CONSERVATI VE | kinase | Human Gene Similar to SWISSPROT- ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa. | 2.70E-51 |

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| 740 | cg43105476 | 702 | GCGAACCCAGT TCGGTCTTCAA AT[G]GGGATT AGCACCTCTAA GTAGCACT | C | T | Asp (1113) | Asn (1114) | CONSERVATI VE | kinasein hibitor | Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6)- HOMO SAPIENS (HUMAN), 168 aa. | 7.80E-86 |
| 741 | cg38642684 | 290 | ATATTCGCCTAGT AATTCTCTGATAA [C/G]ATTAAAGG TATGTAAGTTGC TAGTA | C | T | Asp (1114) | CONSERVATI VE | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]- HOMO SAPIENS (HUMAN), 874 aa. pcds:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS(HUMAN), 874 aa. | 2.60E-50 | |
| 742 | cg39518465 | 864 | CACTTCCTAAAG GAGATGAAGGA AG[G/T]CCTGGG CACCCCTGGCG CAGCCAAT | C | T | Ala (1115) | Val (1115) | CONSERVATI VE | oncogene | Human Gene SWISSPROT- ID:P15498 VAV PROTO-ONCOGENE - HOMO SAPIENS (HUMAN), 846 aa. | 0.00E+00 |
| 743 | cg43021380 | 176 | CAGGCCGGCCCCG GGGGCTGCAGC GCC[G/A]TTAGT GCCACGGCTG TCTATTGTA | G | A | Val (1116) | Ile (1116) | CONSERVATI VE | phosphatase | Human Gene SWISSPROT- ID:Q16849 PROTEIN-TYROSINE PHOSPHATASE N PRECURSOR (EC 3.1.3.48) (R-PTF-N) (PTP IA-2) (ISLET CELL ANTIGEN 512) (ICA 512) (ISLET CELL AUTOANTIGEN 3) - HOMO SAPIENS (HUMAN), 979 aa. | 0.00E+00 |
| 744 | cg39728924 | 365 | CAATTGTGGAG AAGAGTATT AT[G/A]TCGCTA CTCAAGGACCA CTGCTGAG | G | A | Val (1117) | Ile (1117) | CONSERVATI VE | phosphatase | Human Gene Similar to TREMBLNEW-ID:D1024666 PROTEIN-TYROSINE- PHOSPHATASE (EC 3.1.3.48) - MUS MUSCULUS (MOUSE), 426 aa. | 1.20E-64 |

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| 745 | cg42710490 | 851 | CAACCAGCCTAT | G | A | Val | Ile (1118) | CONSERVATI VE | polymera se | Human Gene SWISSNEW-ID:O54888 | 8.90E-172 |
| | | | TGGGGAAAGAA AT[G/A]TCCAGG GTGGAATCCGT TTGGGGAA | | | | | | DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT) - RATTUS NORVEGICUS (RAT), 1135 aa. pcis:TREMBLNEW-ID:G2739048 RNA POLYMERASE I 127 KDA SUBUNIT - RATTUS NORVEGICUS (RAT), 1135 aa. | | |
| 746 | cg44001078 | 316 | GGTTATCAGGA | C | T | Arg | His (1119) | CONSERVATI VE | struct | Human Gene TREMBLNEW- ID:G2920823 CARDIAC MYOSIN BINDING PROTEIN-C - HOMO SAPIENS (HUMAN), 1274 aa. | 0.00E+00 |
| 747 | cg43916919 | 1113 | AGGTAGGAGTC | C | T | Val | Ile (1120) | CONSERVATI VE | struct | Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa. pcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa. | 4.3E-188 2 (2cen) |
| 748 | cg42930605 | 463 | CAGCTCCCTTGCT | C | T | Arg | Lys (1121) | CONSERVATI VE | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 (11p15.5) |
| 749 | cg36824552 | 230 | AAGACGAGGCC | A | G | His | Arg (1122) | CONSERVATI VE | struct | Human Gene Similar to SWISSPROT- ID:Q28046 ADSEVERIN (SCINDERIN) (SC) - BOS TAURUS (BOVINE), 715 aa. | 4E-80 |

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| 750 | cg42522566 | 377 | CAACATCATGAA CCAGCTCAGCC AC[G/A]TAAACTT GATCCAACTTA TGATGC | G | A | Val (1123) | Ile (1124) | CONSERVATI VE | struct | Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa. | 6E-55 |
| 751 | cg42522566 | 509 | GTACACCCTCA CTGAGTTGGAT GT[G/A]TCTTG TTCACCGAGGCA GATCTGTGA | G | A | Val (1124) | Ile (1125) | CONSERVATI VE | struct | Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa. | 6E-55 |
| 752 | cg42489842 | 481 | TGCAAGTGAATA TGCCAAAATACTG CTT[A]CAGAAATA TTAGGAGTTGCA GCTAC | T | A | Ser (1125) | Thr (1126) | CONSERVATI VE | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA(PIG), 704 aa. | 7.3E-106 |
| 753 | cg43919398 | 2201 | GTTAGTCTCTGT GGTGTGCTTATA ATT[C]CATTTGG GGTCCAACATT ACATT | T | C | Ile (1126) | Val (1126) | CONSERVATI VE | transcript | Human Gene SWISSPROT- ID:Q14188 TRANSCRIPTION FACTOR DP-2 (E2F DIMERIZATION PARTNER 2) - HOMO SAPIENS (HUMAN), 385 aa. | 2.7E-202 |
| 754 | cg20612302 | 300 | ATGGAGGGGGC CCACATGGGG CC[A][C]GGCCA TCCTCAAACCTGT CCACGGGC | C | G | Thr (1127) | Ser (1127) | CONSERVATI VE | transcript | Human Gene Similar to SPTREMBL- ID:Q08996 MYELIN TRANSCRIPTION FACTOR 1-LIKE - MUS MUSCULUS (MOUSE), 1182 aa. | 1.7E-53 |
| 755 | cg44928196 | 1474 | GGCTCTGTTCC ATGGAAATTCA TA[G/A]ACACGG GTTTTCTTTAC CATCTA | G | A | Asp (1128) | Asn (1128) | CONSERVATI VE | ubiquitin | Human Gene TREMBLNEW- ID:G2827198 UBIQUITIN PROTEIN LIGASE - MUS MUSCULUS (MOUSE), 854 aa. | 0 |

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| 756 | cg43301812 | 3784 | GGCTGGCCCTT CTCCATGGCTG GGAT[C]GCTCT GCTGGCTTGG TTTGCCCCG | T | C | His (1129) | Arg (1129) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa. | 0.00E+00 | 3 |
| 757 | cg439117191 | 2735 | GCTTCCTCTTTTC ACATTGTATGTA T[C/T]CAGGTGT TCTTGGCAACTCC AAACACA | C | T | Asp (1130) | Asn (1130) | CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA74849 KIAA0826 PROTEIN HOMO SAPIENS (HUMAN), 1236 aa (fragment). | 0.00E+00 | 4 |
| 758 | cg43918356 | 2637 | GCTCATGTCATC TTCATCTAGAAA C[G/A]CCCTCAC GGAATGGAAATT GCTGCC | G | A | Ala | Val (1131) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 0.00E+00 | 12 |
| 759 | cg43932090 | 1186 | TCTTTTCAAGCT TTCCTTATGTTG TTCTATTGCTCT TCATTTCTTGA AGGTTC | T | C | Lys (1132) | Arg (1132) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment). | 0.00E+00 | |
| 760 | cg43950437 | 794 | AGCCAGAGGCT GGTACCTAGAA CCA[G]CTGGAT GGTTCTTGGCT GATGGCGC | G | C | Thr (1133) | Ser (1133) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa. | 0.00E+00 | 12 |
| 761 | cg42935995 | 743 | GCCTGCTCCC CGCTGAGAGC CTC[G]GCCCC TCCAGCCAGCC GTCACTGCT | A | G | Val (1134) | Ala (1134) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa. | 1.00E-274 | |
| 762 | cg43971614 | 2578 | TCCATTGAATC CAATCCCCAT GG[G]CATAAG AAGAGTTCTTC CATAAAAA | A | G | Val (1135) | Ala (1135) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 5.30E-253 | 5 |

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| 763 | cg43922856 | 1581 | CTTGAATTC AGTCACCCATT G[A/G]CAACTAA GGATTCTGTTGCT TGAAAGC | A | G | Val (1136) | Ala (1136) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |
| 764 | cg43922856 | 1783 | CCACCTGTCCAT TCAGTCTCAGTT AT[C]TCCAGCTT GAGAATAGCTCT GATGG | T | C | Ile (1137) | Val (1137) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |
| 765 | cg43955639 | 282 | GGCGGGGG GGATAGCTGCC CAGG[G/C]GTCA GAGGCTCTTG GCTCCTGCCA | C | G | Ser (1138) | Thr (1138) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment). | 2.80E-215 | |
| 766 | cg41022625 | 1121 | CACGGCGTTCT GGATCGTCTCT CC[A/G]TCATTC ACATCATCGCCA CCCTGCT | A | G | Ile (1139) | Val (1139) | CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa. | 2.00E-207 | 11 |
| 767 | cg43119894 | 1960 | TGAGCATAGCT CTGAGCTCTCTT TA[C/T]ACGGTC AGGGTCCACAT AATGCATT | C | T | Val (1140) | Ile (1140) | CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:CAA75235 LACTOSYL CERAMIDE ALPHA-2,3- SIALYLTRANSFERASE (EC 2.4.99.9) - MUS MUSCULUS (MOUSE), 387 aa. | 2.30E-190 | 2 |
| 768 | cg43303845 | 1109 | AGAACGGAGAA GGCTGGAGAGA CTG[C/G]AACGG GAGAGGCAAGA AAGGGAGCG | C | G | Gln (1141) | Glu (1141) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa. | 1.90E-138 | |
| 769 | cg44927166 | 531 | GTCTTGTCTTC CCAATCCCCCTTG G[C/T]GTTCTCG TTCTTATCCCT TTCTCT | C | T | Arg (1142) | His (1142) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBL NEW-ACC:BAA74876 KIAA0853 PROTEIN - HOMO SAPIENS (HUMAN), 967 aa (fragment). | 3.70E-133 | 13 |

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| 770 | cg38059286 | 473 | AGCTGTATAGCT G CCAGTGGTCCCT GA[G/T]CTCCGC CGCTCCCTCTC TCACtGA | T | Glu (1143) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AD39906 FH1/FH2 DOMAIN-CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa. | 4.00E-129 |
| 771 | cg29351416 | 333 | CTGGCCCAGGCCA G GCCCATCCCC TGAG[G/T]GACCT GGCTTTGTCAAT GGGCACCA | T | Glu (1144) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. | 3.20E-127 |
| 772 | cg43960639 | 987 | CCATGTCTGGG A AGAAATGGGAGC CTC[A/C]TCGCC CACTTGAAGTC AAAGTAGA | C | Asp (1145) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC: CAB40416 P24B PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 217 aa. | 9.00E-111 |
| 773 | cg43325007 | 1098 | GTGGATATATGT G GGCTGCAGTA TG[G/A]CCACA GCTTCTCCTGG AGGCTGCC | A | Ala (1146) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa. | 4.80E-110 |
| 774 | cg42907145 | 853 | GCCACCTCCCA G TAACCCTCTAG CA[G/A]CATAGA CTGACTTGCCA CATCGAGG | A | Ala (1147) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50461 LIM DOMAIN PROTEIN, CARDIAC (MUSCLE LIM PROTEIN) (CYSTEINE-RICH PROTEIN 3) (CRP3) (LIM-ONLY PROTEIN 4) - Homo sapiens (Human), 194 aa. | 1.10E-108 |
| 775 | cg43972159 | 1374 | AAGCCATTAGGT A TCTCGGGCTGC TG[A/T]ACTGTT GATTGGACTTT TCTTTC | T | Ser (1148) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa. | 2.60E-102 ⁷ (12q24.1) |

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| 776 | cg39512856 | 508 | CCAGGGCTGTGC CGTTCACACTCT GATTAJATCCC CTCCGGCGAT AACCAAGGT | T | A | Tyr (1149) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 |
| 777 | cg28461713 | 584 | TCTGCAAATTG CTCTGGCAT GG[G(A)CAGCTT GCAGCTGAAGT TGGTTGTA | G | A | Ala (1150) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47710 ALPHA-S1 CASEIN PRECURSOR - Homo sapiens (Human), 185 aa. | 5.90E-96 (4q21.1) 4 |
| 778 | cg43969092 | 361 | CGGGCCCCGTC ATCACGGATGT GCA[CG]GCCC CGTGGTCAGC AGCAGCACA | C | A | Val (1151) | Leu (1151) | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAAT4913 KIAA0890 PROTEIN - HOMO SAPIENS (HUMAN), 1194 aa. | 6.30E-89 |
| 779 | cg426888841 | 487 | GCGTCATAGTAT AAAGAAGGCTT GA[C/T]GACAAA CAG[TCTCTTGCC ATGGTCC | C | T | Val (1152) | Ile (1152) | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 |
| 780 | cg39523553 | 603 | GACGGGTTGGT TCCCGACGAAG ACGIC[T]CCGAG CGGCCAAGTGG GGGTGGCG | C | T | Ala (1153) | Val (1153) | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 |
| 781 | cg39523553 | 819 | ATGGACGTTGGT GCGCAACAGGC CTC[A/G]GGAG TGAAGGTCCAG ATGGCTCTT | A | G | His (1154) | Arg (1154) | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 |

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| 782 | cg39523553 | 857 | CCAGATGGCTCTTCGGCTGCCC[G]AGCTCGATCAGGCATCAAGGTGCCT | G | C | Glu (1155) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 |
| 783 | cg35933325 | 274 | AACCACAGAGAATACAGTGACAACTA[T]AGAACAAAATGACCAAA TGCCACT | A | T | Phe (1156) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA74845 KIAA0822 PROTEIN - HOMO SAPIENS (HUMAN), 1581 aa. | 2.40E-74 |
| 784 | cg41677120 | 544 | GTTGTTAACTTAAGCAATTG[G/A]ATAAAAGTGATTGCAAG GATATGA | G | A | Asp (1157) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 1.10E-71 |
| 785 | cg43951096 | 2850 | AACATCAACATTGTATTGGCTT[C]TATTGGCTCTAGAAGAGTA TCTGG | T | C | Lys (1158) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2.00E-71 |
| 786 | cg42696021 | 444 | GCTGTGCCGCCATTACAATGAAGTG[A/G]ACCGGAAGCTGGCAAG CCTGATT | A | G | Asn (1159) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa. | 1.40E-69 |
| 787 | cg34243633 | 447 | GCTGGCACCGATCATAGAACTTGTTCAGCTGGGAGGAGCA TGGCAAC | T | C | Lys (1160) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. | 1.30E-68 |
| 788 | cg34243633 | 472 | TTCCAGCTGGGCG GAGCAGCATGCAA[C/T]CAGTG TGCCCAAAAGC CCCAGAAGG | C | T | Ile (1161) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. | 1.30E-68 |

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| 789 | cg43942922 | 268 | GTCCTCTGTCAA GACCCCTGAAA CA[G]ATTGTC CCACAGCCCC GAGCTCCA | A Val (1162) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.30E-68 | |
| 790 | cg43942922 | 310 | TGAGCTCCAGC CTTCCACCTCCA CA[G]ACCAGC CTGTCACCTCTG AGCCCAC | A Asp (1163) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.30E-68 | |
| 791 | cg44938009 | 1139 | TTCTGTCAAATGT GGTCCCGTGCCA TG[A]GTTGAA CTGGGATGTCC TCTTCCA | A G Ile (1164) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:O43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO- TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 587 aa. | 5.80E-66 | X |
| 792 | cg39516123 | 631 | AGCCCTCAGGC GGCCACAGAA CAG[T]GGGCA CCAAACACTCC CTAGTCCT | T G Val (1165) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.10E-62 | |
| 793 | cg44921974 | 279 | GATTATGTGCC GTTGAGTTGG TC[A]G[CAGACT TGATGTTTGA AAGTTG | A G Val (1166) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P07148 FATTY ACID-BINDING PROTEIN, LIVER (L-FABP) - Homo sapiens (Human), 127 aa. | 1.6E-61 | 2 (4q28) |
| 794 | cg42731307 | 497 | AAGGCATTGAT GATCCGGTCCC CCA[G/C]TGGGT TGATGGCAAGTT CTGGAATC | G C Leu (1167) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |
| 795 | cg42731307 | 534 | CAAGTCTGGAA TCCTCTGGAAAT CT[G]TCCCCGG TGAGAGTCCCA TTCTCTC | T G Glu (1168) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |

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| 796 | cg44015614 | 1330 | TCCACAACTCT TCTGATGAGATG TT[CCTCCATT CCATGTGTTTG CCAAG | C | Asn C T | Asp (1169) | CONSERVATI VE | UNCLAS IFIED | Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 |
| 797 | cg43298242 | 143 | GATCTGGTGGC AGGGCTCACAG AGA[C]GGGG TGAGGGAGAG ATCGTGGGT | C | Val T | Ile (1170) | CONSERVATI VE | water_ch annel | Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 1.3E-163 |
| 798 | cg43299610 | 842 | CTCCCAGTGCC CGCCCCGACTAC CAC[C]TACATC CACACCGAGAT CTCCCCGGA | C | His T | Tyr (1171) | NON- CONSERVATI VE | ATPase_ associat ed | Human Gene Homologous to SWISSPROT-ID:P39986 PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKERS YEAST), 1215 aa. | 1.40E-109 |
| 799 | cg42532480 | 564 | TTTCCTGAATGA ATGTTAAAGATT CT[TAGTCAAG TCAGTATGGCG ATCCAAG | T | A Arg A | End (1172) | NON- CONSERVATI VE | cadherin | Human Gene Homologous to SWISSPROT-ID:P79995 CADHERIN- 10 PRECURSOR - GALLUS GALLUS (CHICKEN), 789 aa.[pcls:SPTREMBL- ID:P79995 CADHERIN-10 - GALLUS GALLUS (CHICKEN), 789 aa. | 6.00E-115 |
| 800 | cg42926989 | 259 | GCAAATGAGCTG CTGGCAGCACA AAG[G]CTTATC GCACCCAGGAAA GATGCAGC | G | T | Ala Asp (1173) | NON- CONSERVATI VE | cathepsi n | Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa. | 1.7E-136 |
| 801 | cg43991318 | 2521 | TGGTCCGGGAA TACCTGGTGGGA CCCT[G]GGGG CCCGGCTGCCA GGAGCTGCC | T | G | Cys (1174) | NON- CONSERVATI VE | collagen | Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa. | 1.3E-73 (1p34) |

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| 802 | cg43920512 | 1467 | AATTCAAAGTATT CATGGTGTTCT CT[C]CCTAAC CCACCAAGAGAC ACTAAAT | T A | C C | Leu Asn | Pro (1175) (1176) | NON- CONSERVATI VE | cyclin | Human Gene SWISSPROT- ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa. | 4.1E-231 | 4 (4q27) |
| 803 | cg43063374 | 1763 | AGAGATTGAAC GTGTGGTGGC AGA[A]CJACCGG AGCCCCCTGCAT GCAGGACAG | A | T Ser | His (1176) | NON- CONSERVATI VE | cyto450 | Human Gene SWISSNEW-ID:P33259 CYTOCHROME P450 2C17 (EC 1.14.14.1) (CYP11C17) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa.[pcls:SWISSPROT-ID:P33259 CYTOCHROME P450 1C17 (EC 1.14.14.1) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa.] | 3.2E-254 | 10 (10q24.1) | |
| 804 | cg21416244 | 360 | GGGTGAACTGT CTATCCACCAT AT[CT]ATCTATT CAGGCACATT AGGCACCT | C | T Ala | Leu (1177) | NON- CONSERVATI VE | cytochro me | Human Gene Similar to SWISSPROT- ID:P98001 CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) - SACCHAROMYCES DOUGLASSI (YEAST), 534 aa. | 5.5E-69 | | |
| 805 | cg44017721 | 217 | AGATAGGAGTT GAAGGGTGCAGA GGG[C/T]CACGC TGGGCAGGGCG AGCACGAAG | C | T Ala | Thr (1178) | NON- CONSERVATI VE | cytochro me | Human Gene Similar to SPTREMBL- ID:Q00761 CYTOCHROME OXIDASE SUBUNIT VIA HEART ISOFORM PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)) - HOMO SAPIENS (HUMAN), 97 aa. | 2.4E-52 | 22 | |
| 806 | cg43275625 | 1105 | TGGTACTCCCTT GCCGCCAGCTT GG[G]CTCATG GTACACGTTGG GTTGGTA | A | G Ser | Pro (1179) | NON- CONSERVATI VE | deamina se | Human Gene SPTREMBL-ID:Q00465 DSRNA ADENOSINE DEAMINASE DRADA2C - HOMO SAPIENS (HUMAN), 714 aa. | 0 | 21 | |

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| 807 | cg43312829 | 1402 | TAGTGAAATCT CCAAATCAAAGAC A[A/G]CAGGACT CCATGTAACGTGA ATATGA | A G | Thr Ala (1180) | NON- CONSERVATI VE | dehydrog enase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN).617 aa. aa pcis:SWISSPROT-ID:P11586 | 0 | 4 |
| 808 | cg43959136 | 1144 | TGGGCCAACAA GCTTGAGTGCG ATC[C/T]GGTCT GCAATGATGGA GGAATTGCC | C T | Arg Gln (1181) | NON- CONSERVATI VE | dehydrog enase | (METHYLENETETRAHYDROFOLAT E DEHYDROGENASE (EC 1.5.1.5) / METHENYLtetrahydrofolate CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLtetrahydrofolate SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN).934 aa pcis:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLAT E DEHYDROGENASE (EC 1.5.1.5) / METHENYLtetrahydrofolate CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLtetrahydrofolate SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN).934 aa. | 0 | 14 |

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| 809 | cg43969759 | 648 | TGTCAGGGAA AGATCTCATCTG GG[A/G]GTGCC GGATCCCGCC GGATGAC | A C T G | Ile Tyr Val Le | Thr (1182) (1183) | NON- CONSERVATI VE NON- CONSERVATI VE | dehydrog enase dehydrog enase | Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE)- HOMO SAPIENS (HUMAN). 572 aa. | 1.8E-109 | 11 |
| 810 | cg39523614 | 697 | GGGAGCTTAG ACATTGCCACG GATT/CJACGTC CAGAAGGGCAA GCAGTTGG | T C T G | C Tyr Val Phe | His (1183) (1184) | NON- CONSERVATI VE NON- CONSERVATI VE | dehydrog enase dn_a_ma _bind | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-)- MYCOBACTERIUM LEPRAE, 389 aa. | 2.10E-76 | |
| 811 | cg421175288 | 1152 | TGGAGACCCA AAAGTGGGAT TGG[G/T]TTGC CCTAATCCGTCA TGCGAAA | G T T G | A C A Gly | Phe (1184) Cys (1185) | NON- CONSERVATI VE NON- CONSERVATI VE | dn_a_ma _bind | Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBPI6 - HOMO SAPIENS (HUMAN), 592 aa. | 0.00E+00 | 17 |
| 812 | cg43154217 | 1352 | GCAGGAAGGGT GATTGTGAGAG GAC[C/A]AAGAG CTCAGGAACA GCTGGAACT | C A A C | Gly Ala Ala Pro | Gly (1185) (1186) | NON- CONSERVATI VE NON- CONSERVATI VE | dn_a_ma _bind | Human Gene Similar to SWISSPROT- ID:P26599 POLYPRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRP I) (57 KD RNA-BINDING PROTEIN PPTB-1) - HOMO SAPIENS (HUMAN). 531 aa. | 2.20E-90 | |
| 813 | cg39709402 | 108 | GGAAAAACATTA TAAACAAGTGA A[G/C]CCTACAG AGAGGAATCGC AAAAATC | G C C C | Ala Gly Ser | Ala (1186) Cys (1187) | NON- CONSERVATI VE NON- CONSERVATI VE | dn_a_ma _bind | Human Gene Similar to SPTREMBL- ID:Q08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGicus (RAT), 362 aa (fragment). | 3.20E-57 | |
| 814 | cg39709402 | 133 | GCCTACAGAGA GGAATCGCAA AAT[C/G]CCTGA AAGAAATTCCAG GAAAACACA | C C C C | G G G G | Ser Ser Ser Ser | NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE | dn_a_ma _bind | Human Gene Similar to SPTREMBL- ID:Q08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGicus (RAT), 362 aa (fragment). | 3.20E-57 | |

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| 815 | cg39709402 | 57 GATGCTGGAGG A ACTTCAAGAAAG AC[AG]TGAAAGA ACTCCCTTAGAG AACACAA | G Met (1188) | Val (1189) | NON- CONSERVATI VE | dna_ma _bind | Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment). | 3.20E-57 |
| 816 | cg39709402 | 76 AAAAGACATGAA A GAACCTCCCTTAG AG[G]AACACA GGAAAACATTA AAACAA | G Glu (1189) | Gly (1189) | NON- CONSERVATI VE | dna_ma _bind | Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment). | 3.20E-57 |
| 817 | cg39709402 | 94 CTTAGAGAAACA A CAGGGAAAACATT A[A]G]TAAACAA GTAGAAAGCCTA CAGAGAG | G Asn (1190) | Ser (1190) | NON- CONSERVATI VE | dna_ma _bind | Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment). | 3.20E-57 |
| 818 | cg39709402 | 96 TAGAGAAAACACA A GGAAAAACATTAA T[T/G]AACAAAGT AGAACGCCTACA GAGAGGA | G Lys (1191) | Glu (1191) | NON- CONSERVATI VE | dna_ma _bind | Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment). | 3.20E-57 |
| 819 | cg43950268 | 1949 TTGCTATGTCC G TCCTTGACCTCC T[G/A]CTCGGTG GGGGTCACAAT GCCCTCC | A Gln (1192) | End (1192) | NON- CONSERVATI VE | eph | Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa. | 0.00E+00 |
| 820 | cg43985169 | 540 AAGACGAAATGG T GTGGTGGTAGA GATT[C]CTGAA GAAATGAAATA GATGGTGA | C Ser (1193) | Pro (1193) | NON- CONSERVATI VE | eph | Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa. | 2.40E-123 |
| 821 | cg43997616 | 2250 AAAGCCAGCGG T AGCCGTAAGCA TCATTCACTGCT TCCTCTTCACT CATCACT | C Tyr (1194) | Cys (1194) | NON- CONSERVATI VE | eph | Human Gene Similar to TREMBLNEW-ID:G2735762 HEAT SHOCK PROTEIN DNAJ - LEPTOSPIRA INTERROGANS, 369 aa. | 1.40E-55 |

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| 822 | cg43319420 | 992 | CACGACAACTA | T | C | Phe | Ser (1195) | NON- CONSERVATI VE | esterase | Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC- NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.[pcds:SWISSPROT-ID:Q23917 3',5' CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. | 3.30E-60 | 21 |
| 823 | cg44034764 | 382 | GAGGTCCAGGC | T | C | Glu | Gly (1196) | NON- CONSERVATI VE | glycoprot ein | Human Gene SWISSPROT- ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-)- HOMO SAPIENS (HUMAN), 732 aa. | 0.00E+00 | 7 (Xp21.2) |
| 824 | cg43991224 | 217 | TCTCATCTGTCT | T | A | Val | Asp (1197) | NON- CONSERVATI VE | glycoprot ein | Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa. (fragment). | 1.50E-139 | |
| 825 | cg44018623 | 1824 | TGGTACGCT | G | A | Pro | Leu (1198) | NON- CONSERVATI VE | glycoprot ein | Human Gene Homologous to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.90E-114 | 6 |
| 826 | cg38924741 | 598 | AAAGAGGAGAA | T | C | Leu | Ser (1199) | NON- CONSERVATI VE | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P04196 HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG) - HOMO SAPIENS (HUMAN), 525 aa. | 3.30E-55 | |

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| 827 | cg43322513 | 13082 | TTCCCTGTTCTTC ACATGGTGAGC CC C TGGCCTG CTGCTGCTTGC ATTGGGG | C T | Arg Ser | Gln (1200) (1201) | NON- CONSERVATI VE NON- CONSERVATI VE | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE- RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa. | 3.30E-54 | 12 |
| 828 | cg44913214 | 2306 | GAACACAACAAA GAAAAAAACAGA GT[G]TGGGAC TCATCCAAAAGG GACGAGA | C T | Phe (1201) | NON- CONSERVATI VE | helicase | Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa. | 0.00E+00 | 10 | |
| 829 | cg39529972 | 278 | TTGGCCTCGAC ATCATTCCCTGA CG A/G GGACTT AAAGGGTAGCA ATTGGTAT | A G | Ser (1202) | Pro (1202) | NON- CONSERVATI VE | hydrolas e | Human Gene Similar to SWISSPROT- ID:Q01477 UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 3) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 3) (DEUBIQUITINATING ENZYME 3) - SACCHAROMYCES CEREVISIAE (BAKERS YEAST), 912 aa. | 1.00E-52 | |
| 830 | cg43925670 | 2309 | TAGTTTGCCCAA ACAGGCATCAC CT[G]GGAACT TTCTTCCATCA AGTCAGC | C G | Arg (1203) | Pro (1203) | NON- CONSERVATI VE | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR)- HOMO SAPIENS (HUMAN), 729 aa. pcts:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0.00E+00 | 1 |

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| 831 | cg43925670 | 2369 | TTTGTCACTC TTCTCTCATT TA[G]AAATTAAAGT TTAAATCGTTG CTCAG | A | G | Leu | Ser (1204) | NON- CONSERVATI VE | Interfero n |
| | | | | | | | | | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR)- HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) |
| | | | | | | | | | 0.00E+00 |
| 832 | cg43925670 | 2458 | CCTCTAATCCCT TTAGTAGAACAA TG[G]TTCTTGT TTTTTTCCCAT CTTTA | G | T | Asn | Lys (1205) | NON- CONSERVATI VE | Interfero n |
| | | | | | | | | | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR)- HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) |
| | | | | | | | | | 0.00E+00 |
| 833 | cg43925670 | 2467 | CTTTTAGAGAA CAATGTTCTTGT AT[G]TTTTCC CATCTTACAGA CATAA | T | G | Lys | Asn (1206) | NON- CONSERVATI VE | Interfero n |
| | | | | | | | | | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR)- HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) |
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| 834 | cg43331742 | 845 | TCCCTGAGGTG CTTCCCACAGA CTCG[A]ATTCT GAGTTTCCACA GAAAAGA | G | A | Ser | Leu (1207) | NON- CONSERVATI VE | isomeras e | Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPROPIONYL-COA EPIMERASE (EC 5.---) - RATTUS NORVEGICUS (RAT), 361 aa. | 5.60E-131 |
| 835 | cg43253796 | 1812 | GAAATGGATCTT ATTGGACCTTG C[G/T]ACAAAGAC TGCCTGGAGAT TTTCCCAC | G | T | Arg | Leu (1208) | NON- CONSERVATI VE | kinase | Human Gene SWISSNEW-ID:P42338 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K)- HOMO SAPIENS (HUMAN), 1070 aa;Ipcis:SWISSPROT-ID:P42338 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K)- HOMO SAPIENS (HUMAN), 1070 aa. aa;SPTREMBL-ID:Q60680 PHOSPHATIDYLINOSITOL 3- KINASE P110 SUBUNIT BETA (PTDINS-3-KINASE P110) (PI3K)- HOMO SAPIENS (HUMAN), 1070 aa. aa;SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa. | 0.00E+00 |
| 836 | cg43257400 | 2094 | GACATCAGCAT GGCTGCCCG ACTT[C]CAGCA GAACATGATCAT | T | C | Ser | Pro (1209) | NON- CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa. | 0.00E+00 |
| 837 | cg43974480 | 686 | TCA CGG GACT TTG GACT GTGCC AAAA T[G/T]GG CCT CA TGAG CCT GACA ACGAACT | G | T | Met | Ile (1210) | NON- CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q000114 HYPOTHETICAL HUMAN SERINE- THREONINE PROTEIN KINASE R31240_1 - HOMO SAPIENS (HUMAN), 1237 aa (fragment). | 0.00E+00 |
| 838 | cg43922705 | 4337 | CAAACGGGCTTT CTCCATGGTGC CC[T/C]GCCAAA CCCTGGAGTC CCAGGCTG | T | C | Gin | Arg (1211) | NON- CONSERVATI VE | kinase | Human Gene SWISSPROT- ID:P27987 1D-MYO-INOSITOL- TRISPHOSPHATE 3-KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5- TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 505 aa (fragment). | 3.80E-279 1 (1q41) |

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| 839 | cg38438124 | 1460 | TGCAAAACTGT TAAACATGGCG CT[G/C]GGCGG AGATCTCCACCC GTGAACCC | G C Gly (1212) | Arg (1212) | NON- CONSERVATI VE | kinase | Human Gene SWISSPROT-ID:O70172 PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE)- MUS MUSCULUS (MOUSE), 405 aa. | 2.80E-216 | 10 |
| 840 | cg42703622 | 385 | GTATGCAGCAA CAAGAGCAACT CTG[A/G]AGAAC GAATTGGAGG TGGCCACAT | A G Lys (1213) | Glu (1213) | NON- CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa. | 3.00E-187 | 14 |
| 841 | cg42703622 | 395 | ACAAGAGCAAC TCTGAGAAGG AATT/CCTGGAG GTGCCACATT AAAGATGAA | T C Phe (1214) | Ser (1214) | NON- CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa. | 3.00E-187 | 12 |
| 842 | cg41501665 | 96 | GAGTACACCAT CAAGTCGCACT CCA[G/A]CTTGC CGCCCAACAAAC AGCTACGCC | G A Ser (1215) | Asn (1215) | NON- CONSERVATI VE | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 | |
| 843 | cg25143358 | 457 | GCTTATGGGT TCGACATCCAAT G[C/T]GTGATG TCCTCCACAAAC TCCACG | C T Ala (1216) | Thr (1216) | NON- CONSERVATI VE | kinase | Human Gene Similar to SWISSPROT- ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa. | 2.70E-51 | |
| 844 | cg29023997 | 179 | TGCATGGTTCC ATTTCATCTG G[A/G]TGGGATG GAGCACCATGT GCGCACC | A G Asp (1217) | Gly (1217) | NON- CONSERVATI VE | kinase receptor | Human Gene SWISSPROT- ID:P36896 SERINE/THREONINE- PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37) (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB) - HOMO SAPIENS (HUMAN), 505 aa. | 9.30E-280 | 12 |

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| 845 | cg43975720 | 3917 | CATCCACCCAG CCCAGATGAC CGG[A]C]CCTT TACCAATTGAG GCTGCGTG | A | C | Thr (1218) | Pro (1218) | NON- CONSERVATI VE | kinesin | Human Gene SWISSPROT- ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa. | 0.00E+00 | 2 |
| 846 | cg44013875 | 1710 | GCCATGGAGAG GCTGCAGGAGA CAG[G]GAAGA TTATAGCTGAGC TGAAACGAG | A | G | Glu (1219) | Gly (1219) | NON- CONSERVATI VE | kinesin | Human Gene SWISSNEW-ID:Q43896 KINESIN-LIKE PROTEIN KIF1C- HOMO SAPIENS (HUMAN), 1103 aa. pcis:TREMBLNEW-ID:G2738149 KINESIN-LIKE MOTOR PROTEIN KIF1C - HOMO SAPIENS (HUMAN), 1103 aa. | 0.00E+00 | |
| 847 | cg44009224 | 2806 | TTGGATCCTGA AAATGTTGATT TT[C]ATGTTGGA GGTTACCCACC TGATT | T | C | Tyr (1220) | His (1220) | NON- CONSERVATI VE | laminin | Human Gene SWISSPROT- ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa. | 0.00E+00 | |
| 848 | cg42930646 | 1228 | TGATGCCGATA GGCTATGGATG GAA[A]GTTGGAC GATGAGGAGGA CCTGCCCTTC | A | G | Met (1221) | Val (1221) | NON- CONSERVATI VE | laminin | Human Gene SWISSPROT- ID:P07221 CALSEQUESTRIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN)- ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa. | 1.80E-198 | 1 |
| 849 | cg43935885 | 3745 | CCAGACAGCAC CACTGGAACCC CTC[C/T]TAGCA GGCACCCAGAC CCGAAGAAC | C | T | Pro (1222) | Leu (1222) | NON- CONSERVATI VE | MHC | Human Gene SPTREMBL-ID:P79457 MALE-SPECIFIC HISTOCOMPATIBILITY ANTIGEN H- YDB - MUS MUSCULUS (MOUSE), 1186 aa. | 7.20E-173 | |
| 850 | cg42928872 | 1807 | GAGCTGCAGAG GAGGCTGGACC AGT[C/T]CATTG GGAAGGCCCTCA CTGTTCATC | C | T | Ser (1223) | Phe (1223) | NON- CONSERVATI VE | misc_ch annel | Human Gene TREMBLNEW- ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K ⁺ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa. | 0.00E+00 | 11 |

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| 851 | cg44019843 | 929 | GAGTGACCCGC CTCCTGGTC AAG[T]ATGTTG GAGTACACCTC ACAGGGAT | A T Asn (1224) | Tyr (1225) | NON- CONSERVATI VE | misc_ch annel | Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa. | 0.00E+00 (17q23.1) | 17 |
| 852 | cg44128805 | 1396 | AGTGCACACAG TGAGCTCAGAG CTTIC/TCCCCCT GAAAACCAGAA GTTCAACT | C T Glu (1225) | Lys (1225) | NON- CONSERVATI VE | nuclease | Human Gene Similar to SWISSPROT- ID:P54278 PMS1 PROTEIN HOMOLOG 2 (DNA MISMATCH REPAIR PROTEIN PMS2) - HOMO SAPIENS (HUMAN), 862 aa. | 1.60E-76 | 7 |
| 853 | cg38642684 | 304 | TTTCGTATAATC ATTAAAGGTATG T[A]TAGTTGCTA GTATTTAATTAA ACCTT | A T Leu (1226) | End (1226) | NON- CONSERVATI VE | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |
| 854 | cg38642684 | 417 | CTTTTCAGGTG CAATGATTAAC CIATCTTAACTG TGCAATTCTTAT GACAG | A T Ser (1227) | Arg (1227) | NON- CONSERVATI VE | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |

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| 855 | cg44913844 | 1194 | CCAGTTGGTAAAG CTGGCTCTAAC C[G/A]GAATCCA GTTAATTACCTT GCTGAG | G | A | Arg (1228) | Gln (1228) | NON- CONSERVATI VE | peroxida se | Human Gene SWISSPROT- ID:P04040 CATALASE (EC 1.11.1.6)- HOMO SAPIENS (HUMAN), 527 aa. | 2.70E-296 (11p13) | 11 |
| 856 | cg40084915 | 5005 | CCTCGGGTCTG GGGAGATGAGG GCCCT[C]CAAAC AGCACCTGATAT TCATTGGG | T | C | Glu (1229) | Gly (1229) | NON- CONSERVATI VE | phosphatase | Human Gene SPTREMBL-ID:Q00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa. | 0.00E+00 | 1 |
| 857 | cg42720088 | 214 | AAAGCTCAGAG AGATCTGGCT ATG[A/T]GCCAC TTGTCA[GCT]G GAGGAAGCC | A | T | Glu (1230) | Val (1230) | NON- CONSERVATI VE | reductase | Human Gene Similar to SWISSPROT- ID:P22072 3 BETA-HYDROXYSTEROID DEHYDROGENASE/DELTA 5->4- ISOMERASE TYPE II (3BETA-HSD II) (3-BETA-HYDROXY-DELTA5- STEROID DEHYDROGENASE (EC 1.11.1.145) (3-BETA-HYDROXY-5- ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE) / STEROID DELTA-ISOMERASE (EC 5.3.3.1) (DELTA-5-3-KETOSTEROID ISOMERASE) - RATTUS NORVEGICUS (RAT) 372 aa | 2.40E-50 | |
| 858 | cg43957486 | 1528 | CGCTCCTGCAC CGCATCCGGA CG[A/T]GTCCCT GCAACGACCTC TGGAGCAC | A | T | Gln (1231) | Leu (1231) | NON- CONSERVATI VE | struct | Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETTOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa. | 0.00E+00 (20p11.2) | 20 (20p11.2) |
| 859 | cg40148056 | 1462 | CTCAGAGACCC CTAACAAACCA GCA[G/C]CCACA GAGGGAAACAC TTAAGGATC | G | C | Gln (1232) | His (1232) | NON- CONSERVATI VE | struct | Human Gene SPTREMBL-ID:Q92777 SYNAPSIN IIB - HOMO SAPIENS (HUMAN), 478 aa. | 2.90E-260 | 3 (3p) |

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| 860 | cg43981852 | 473 | CACCTCCCTCCA GCTTCCCAGCC TCC[CT]CGGGCT CTGGCCAGGCT GCCGCTGGG | C | T | Gly (1233) | Glu (1233) | NON- CONSERVATI VE | struct | Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa. | 7.80E-113 |
| 861 | cg42522566 | 318 | GCAGCCAAGAT CATCAAAGTGA GA[N/G]CGTAAA GGACCGGGAGG ATGTGAAG | A | G | Asn (1234) | Ser (1234) | NON- CONSERVATI VE | struct | Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa. | 6.00E-55 |
| 862 | cg43297806 | 966 | ATAGTAGCCAG GGACAAGACAG CGGT[C]TCTGC AGGGAGCGTAG TGCCAGAGG | T | C | Asn (1235) | Ser (1235) | NON- CONSERVATI VE | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N-HEPARIN SULFATE (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. Ipcis:TREMBLN1NEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa | 0.00E+00 |
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| 863 | cg43297806 | 994 | TGCAGGGAGCG GGGT[C]CTGGG AGGAGGCTGAA ATCACCTGA | T | C | Thr (1236) | Ala (1236) | NON- CONSERVATI VE | sulfotran sterase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N-HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. [pcis:TREMBLNW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa. | 0.00E+00 | 10 |
| 864 | cg43987111 | 1337 | AGTAGTCTGCG TCTCCATAGAGT TT[CA]CTCATGA CTGAGTTCTGG TCTGGAA | C | A | Arg (1237) | Ser (1237) | NON- CONSERVATI VE | synthase | Human Gene SWISSPROT- ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa. | 0.00E+00 | 18 (1p34.1) |
| 865 | cg43976335 | 633 | GAAAATGCACTG GACCACTCGGG CAG[G/A]GCTGC CAGGCCGTAGC AGGCAATTG | G | A | Pro (1238) | Ser (1238) | NON- CONSERVATI VE | synthase | Human Gene SWISSPROT- ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa. | 5.30E-240 | 20 (20q11.2) |
| 866 | cg39515668 | 605 | ACGCACGAACC GGTCATACTGG TCGG[T]TGATC CAGGAACGGTC GCACAGCTG | G | T | Thr (1239) | Asn (1239) | NON- CONSERVATI VE | synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.80E-72 | |
| 867 | cg44027791 | 1261 | GAAGCGCTTCT GACACTGGGG CAC[T/C]CGAAG CGTTTGTCCCC GTGGGGT | T | C | Glu (1240) | Gly (1240) | NON- CONSERVATI VE | transcript Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa. | 0.00E+00 | 17 | |

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| 868 | cg43992817 | 578 | GAGGGCCGCT GGAAGGTGACA CTGCCTGTTGG GCCACGGAG GTGCCGCTG | C | T | Ala | Thr (1241) | NON- CONSERVATI VE | transcript factor | Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN). 280 aa. | 1.50E-144 | 3 |
| 869 | cg43297259 | 816 | TAAGTGTCTGAT GAGGTGTGACT TCCTCGGCTAA AGCCCTTGCTCA CACTCCCT | C | Gln | Arg (1242) | | NON- CONSERVATI VE | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 7.80E-54 | |
| 870 | cg42716761 | 1594 | CGAGAAGACCC TATACCATCACG TGCGGACGGCT GCGACGTGTT CACCTCCG | C | G | His | Asp (1243) | NON- CONSERVATI VE | transcript factor | Human Gene SWISSNEW-ID:Q61079 SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM) - MUS MUSCULUS (MOUSE), 657 aa. pcds:SWISSPROT-ID:Q61079 SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM) - MUS MUSCULUS (MOUSE), 657 aa. | 5.7e-312 | 21 |
| 871 | cg42166807 | 2828 | AGAGCAATGGC TCTCTTCACTCC GT[G/A]GAAGTT GTCCTCTCAGAA GCTGGGC | G | A | Trp | End (1244) | NON- CONSERVATI VE | transferase | Human Gene SWISSPROT- ID:Q09328 ALPHA-1,3(6)- MANNOSYLGLYCOPROTEIN BETA- 1,6-N-ACETYLYL- GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSE BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFE RASE) (N-ACETYLGLUCOSAMINYL- TRANSFERASE V) (GNT-V) (GLCNAC-T V) - HOMO SAPIENS (HUMAN). 741 aa. | 0.00E+00 | 2 (2q21) |

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| 872 | cg38869466 | 752 | TTCACTTGTATT AACGTCCTGGT CC[T/C]GGGCTT CATTAATGGTGT AGGATT | T | C | Leu | Pro (1245) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:P30825 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG) - HOMO SAPIENS (HUMAN), 629 aa. | 0.00E+00 | 13 |
| 873 | cg42742340 | 3392 | CAGGAGACGG TGTCATCAGCA TC[CT]GGGCCT CCCTGCAGCAG ACCAGGC | C | T | Arg | Trp (1246) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:Q04671 P PROTEIN (MELANOCYTE-SPECIFIC TRANSPORTER PROTEIN) - HOMO SAPIENS (HUMAN), 838 aa. | 0.00E+00 | 1 |
| 874 | cg43976701 | 513 | TGGTATATCTGA ACTGAATCAGC CT[G/C]CTGAAC TTTACCTCAGT TTCTTAG | G | C | Ala | Pro (1247) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa. | 0.00E+00 | |
| 875 | cg43920728 | 2024 | GTAAGTCCTATT GTAATAATTGTG C[A/G]TGAGCAG TGCTGGGAGT TGACAGC | A | G | Cys | Arg (1248) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa. | 2.90E-237 | 1 (1p31) |
| 876 | cg43920728 | 2185 | TGCTTGCTCTG GAAGGGCAGAG TGC[C/T]GCTCA CCTCCCTTTAGC CAAAGTAA | C | T | Arg | Gln (1249) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa. | 2.90E-237 | 1 (1p31) |

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| 877 | cg42339179 | 450 | TCCTCCACCAAG GGTCA[TTTGCG GT[G/A]TTAAAA GTTCCAGTGATC TCAATG | G | A | His (1250) | Tyr (1250) | NON- CONSERVATI VE | Transport | Human Gene Homologous to SWISSNEW-ID:Q60714 LONG- CHAIN FATTY ACID TRANSPORT PROTEIN (FATP) - MUS MUSCULUS (MOUSE), 646 aa.[pc:SWISSPROT- ID:Q60714 LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP) - MUS MUSCULUS (MOUSE), 646 aa. | 1.90E-105 | 15 3 |
| 878 | cg17663981 | 383 | TGCACCTGCAG CCAAAAACCT GCAG[A]CTGCC CCAAGGGAT GTCAAATAC | G | A | Ser (1251) | Asn (1251) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa. | 0.00E+00 | 10 (10p11.2) |
| 879 | cg43918356 | 1806 | GCTCCCGTAG CGGGGCTGTAG CGC[C/T]CAGGA CTGGCCAGGCC TGGCTTTGC | C | T | Gly (1252) | Glu (1252) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 0.00E+00 | 12 |
| 880 | cg43924089 | 1080 | ACCTCCTGGAG CAGCTCTGGTG TTA[C/T]ATTCCC TGCCCCCTGGAG TTCCCACT | C | T | His (1253) | Tyr (1253) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:BAA31589 KIAA0614 PROTEIN HOMO SAPIENS (HUMAN), 1630 aa (fragment). | 0.00E+00 | 12 |
| 881 | cg43930961 | 2459 | TTCTCCGTAGT CACAGACGTTA GG[C/T]TACTGCC TTTCGGCTTCAA TGGAAAC | C | T | Ser (1254) | Asn (1254) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:BAA20772 KIAA0313 PROTEIN HOMO SAPIENS (HUMAN), 1499 aa. | 0.00E+00 | 4 |
| 882 | cg43966528 | 680 | AACAAACACATTCA AGTACAGTGCA GC[G/T]ATCAG CAGGCCAAGTT AACCAATC | A | G | Met (1255) | Thr (1255) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O00237 HKF-1 - HOMO SAPIENS (HUMAN), 685 aa. | 0.00E+00 | |

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| 883 | cg43980727 | 1367 | TCCTCCCTTGTA GTCAGAGACAT CA[G/A]GAGAGT AACTGGATGTAA GCTCCAA | G | A | Pro (1256) | Leu (1256) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa. | 0.00E+00 | 17 |
| 884 | cg43981483 | 1540 | TGACTGCATTAT TCGAGCTGCT TA[A/G]GGACAA ATTCTACCTTCT TCTGGGT | A | G | Leu (1257) | Pro (1257) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75882 ATTRACTIN - HOMO SAPIENS (HUMAN), 1198 aa. | 0.00E+00 | 20 |
| 885 | cg44932392 | 1200 | TAGATGAAGGA GCCTGAGTAAG AGG[C/T]CACGC ACCAGCCTGTA GAACATATA | C | T | Trp (1258) | End (1258) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa. | 0.00E+00 | |
| 886 | cg44932924 | 2754 | AACAGTGAGTC GGTCCAGCAGC AGA[T/C]GGAGT TCTTGAAACAGG CAGCTGTTG | T | C | Met (1259) | Thr (1259) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92574 HAMARTIN (MYELOBLAST KIAA0243) - HOMO SAPIENS (HUMAN), 1164 aa. | 0.00E+00 | 9 |
| 887 | cg43985955 | 2082 | ACCTCCAAACC CCTTGGCCCT GTAT[C]CAGGA GCACAGATACA GTTTATGTA | T | C | Ser (1260) | Pro (1260) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 | |
| 888 | cg44002507 | 1373 | GTGCCACTTGG CAGCCAGCAGG ATC[C/T]GGCT ATGTTCCACGCA GCCGGAGAA | C | T | Gly (1261) | Glu (1261) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa. | 8.10E-298 | |
| 889 | cg44002507 | 2870 | TTTCCTTCCCT TTGAGAAAATTTC TT[C/T]CTTAATGC TGGATTCCGAA CTCAGG | T | C | Lys (1262) | Glu (1262) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa. | 8.10E-298 | |

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| 890 | cg44002507 | 507 | CGCAGGGTCTG GTGGCCATGA ACAC[C]GCGCA CGGGCACCAAGG TTGGGCTCG | C | T | Val (1263) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- SAPIENS (HUMAN), 1001 aa. | 8.10E-298 |
| 891 | cg44128920 | 1086 | GAGCAGCAGCG AAAACGGCTTC AC[A/C]GCGATT GGAAGAACGCA GTGTTGAA | A | C | Gln (1264) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa. | 1.00E-290 |
| 892 | cg43968641 | 3315 | TCATTCCATCTCA GGGAACATATC AG[CT]CAGAGA AATAACAAGAA CATTCCT | C | T | Ala (1265) | Thr (1265) | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment). | 2.00E-285 |
| 893 | cg43934178 | 2180 | ACAAAGTAGTG GAACCTCCCTCTT GA[G]CACGTC CAGGGTGTGGC CCAGGGACC | A | G | Phe (1266) | Leu (1266) | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa. | 1.80E-274 |
| 894 | cg43934178 | 2596 | CCAGGGCATGA CCTCCGGTGAAG CCTTG[A]GTGAG AGGACGGTCTT CCGGGAGCA | G | A | Pro (1267) | Leu (1267) | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa. | 1.80E-274 |
| 895 | cg43949042 | 378 | GGACGTACATG AGGACGGCTAT TGGC[C]ATGTGC GATGATGAGGC ACAGCCACA | C | A | Gln (1268) | His (1268) | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa. | 6.10E-268 |
| 896 | cg43916582 | 2097 | CCTTCATCTTA TTCTGCTGCTCA G[T]GTTCCATT GTTCCCTTGAT TGCGT | T | G | Thr (1269) | Pro (1269) | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75475 LENS EPITHELIUM- DERIVED GROWTH FACTOR - HOMO SAPIENS (HUMAN), 530 aa. | 2.30E-259 |

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| 897 | cg43258841 | 485 | AACTCCATCCAC AAGTCCTTGTG A[A/G]TAATCAAT CGCTGAGCCTC ATCTCT | A | G | Ile (1270) | Thr (1270) | NON- CONSERVATI VE | SIFIED | UNCLAS | Human Gene SWISSNEW- RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN)- Homo sapiens (Human), 540 aa. | 2.70E-258 | |
| 898 | cg43979679 | 619 | GAGAAGGAGGCC CGGGAAAGTGT GACIC[TAGGAG AAACGGGCAC CAGCTTTGC | C | T | Gln (1271) | Non- CONSERVATI VE | UNCLAS | Human Gene SPTRMBL- ACC:Q13977 MAJOR YO PARANEOPLASTIC ANTIGEN - HOMO SAPIENS (HUMAN), 509 aa (fragment). | 5.60E-258 | 16 (16p13.1) | | |
| 899 | cg42202923 | 887 | TACCCCATTGGT CTTCAGGCCCTG C[A/G]GCAGCTC CGATGAGGTCA GCTGCCG | A | G | Leu (1272) | Pro (1272) | NON- CONSERVATI VE | SIFIED | UNCLAS | Human Gene SPTRMBL - ACC:O75926 PROTEIN INHIBITOR OF ACTIVATED STAT PROTEIN PIASY - HOMO SAPIENS (HUMAN), 510 aa. | 2.40E-256 | |
| 900 | cg43320405 | 994 | CCAGGGCTCGA ATGGACAGCAC CTT[C/A]ATGATG GGGTGGTGGTG GCTCAGGGC | C | A | Met (1273) | Ile (1273) | NON- CONSERVATI VE | SIFIED | UNCLAS | Human Gene TREMBL NEW- ACC: CAB46424 DKFZP434G153 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 8.20E-245 | |
| 901 | cg43917689 | 3689 | TGACAAACGGAG GCTCAGGGGT TGT[G/A]GCTGA TCTTCAGAAC TCAAGCCA | G | A | His (1274) | Tyr (1274) | NON- CONSERVATI VE | SIFIED | UNCLAS | Human Gene SPTRMBL - ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa. | 3.50E-240 | 3 |
| 902 | cg43922856 | 1546 | GAGAATTCA GATTGGCAGAA TAG[G/A]AGATG CATGCTTGA TTCCAGTC | G | A | Pro (1275) | Ser (1275) | NON- CONSERVATI VE | SIFIED | UNCLAS | Human Gene SWISSPROT- ACC:P42167 THYMOPOETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |
| 903 | cg43922856 | 1608 | AACTAAGGATTCA GTTGCTTGAAG CC[A/T]TTATAGT TTCAGCTATGG GAGTACT | A | T | Met (1276) | Lys (1276) | NON- CONSERVATI VE | SIFIED | UNCLAS | Human Gene SWISSPROT- ACC:P42167 THYMOPOETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |

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| 904 | cg43955639 | 505 | CGTTGGCAGG CATGGTGATGA GGG[G/A]TGCTG GGCCAGGGAG GTGGCAGGA | G | A | Pro (127) | Ser (127) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment). | 2.80E-215 |
| 905 | cg43950766 | 991 | AGGAATGACCA T AAGCACCTGGG TCAT[CT]ACTTGT CCACCCACTCTT TAATT | C | Tyr (1278) | Cys (1278) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:ADD44491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa. | 5.30E-214 | |
| 906 | cg43985159 | 2102 | ACTTCTGCCTC G AGCTGCAAACC CA[G/A]AGGACG GCATCCGAGGA CTGAACGC | A | Ser (1279) | Phe (1279) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15018 ORF - HOMO SAPIENS (HUMAN), 419 aa (fragment). | 1.30E-212 | |
| 907 | cg41022625 | 1136 | CGTTCTCCAT G CATTCACATCAT CT[G/T]CCACCT GCTCTCAGCA CGCAAGCT | T | Ala (1280) | Ser (1280) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:ADD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa. | 2.00E-207 | |
| 908 | cg44002669 | 1438 | ACCTTGGCTT C GCACTGGGG AGC[C/T]CCGT CCAGTTCCT TCTCCCTC | T | Gly (1281) | Ser (1281) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa. | 8.80E-205 | |
| 909 | cg44128902 | 675 | CGGGATCGAG ACAGAGACAGA GAG[G/C]GGGAC AGGGATCGGGA TCGGATCG | C | G | Arg (1282) | Gly (1282) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa. | 1.00E-201 |
| 910 | cg44129213 | 1413 | GGGTGGACT T GGCTGCAGATG TCAT[CT]TGTAA TTCAAGATTCTT CTGGCGA | T | C | Met (1283) | Val (1283) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O88466 ZINC FINGER PROTEIN 106 - MUS MUSCULUS (MOUSE), 1888 aa. | 5.60E-194 |

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| 911 | cg43996402 | 684 | CTTCTCCGGCT CCTTCCCTCC GC[A]GTGGCT TCTGCTGCTCC CCTCCCTT | C | A | Gly (1284) | Cys (1284) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.60E-189 | 2 |
| 912 | cg43984909 | 1268 | CGA[TATCAGCT GCATCCAGTG CC[C/T]CAGACG AGAATAACAAGC CAAGGCCCT | C | T | Pro (1285) | Leu (1285) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q99963 PROTEIN CONTAINING SH3 DOMAIN, SH3GL3 - HOMO SAPIENS (HUMAN), 347 aa. | 1.70E-187 | 15 |
| 913 | cg42910688 | 778 | GACAGAGGACA TTCCCATATAATT TG[G/T]TTGGCA ACAAAAGTGA CTAGTGGCG | G | T | Val (1286) | Phe (1286) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P55040 GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa. | 7.70E-158 | 8 |
| 914 | cg43950590 | 1351 | AAGAATCCTCC GACGGCTTCGT TAC[C/T]ATCCTG TCTGAAGGGAA TTGCACGA | C | T | Gly (1287) | Ser (1287) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 915 | cg44931503 | 945 | TTTAAGAGTT CATATAATCATA G[A/G]GGCTTC AAATACCGTTGT TCCTTC | A | G | Leu (1288) | Pro (1288) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34078 CGI-83 PROTEIN - HOMO SAPIENS (HUMAN), 288 aa. | 5.00E-154 | |
| 916 | cg43303845 | 774 | ACATTGCCTAGA TCAAACCTCACAA CTT/CACCTGCT CAAGTTCAAAT GGCCCA | T | C | Leu (1289) | Pro (1289) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa. | 1.90E-138 | |
| 917 | cg43973762 | 117 | AGCTGAACAAC AGAAGTTGG AAT[G/T]AGGAG TTAAAATATGCC AGAGGCAA | G | T | Glu (1290) | End (1290) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.20E-137 | |

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| 918 | cg43973762 | 165 | CAAAGAACATA TTGAAACACAAT TA[G/C]CAGAGT ATCACAAATTGG CTAGAAA | G | C | Ala (1291) | Pro (1291) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.20E-137 |
| 919 | cg43973762 | 376 | GCCCTAAATAAA AAAATGGGTTG G[A/G]GGATACT TTAGAACAAATTG AATGCA | A | G | Glu (1292) | Gly (1292) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.20E-137 |
| 920 | cg42910848 | 443 | CCATGGTGCCA GGCGTGCTCC CCAG[C]GTGCC TCCCCGGGTGCT GAAGATCTT | G | C | Pro (1293) | Arg (1293) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment). | 3.10E-132 |
| 921 | cg29351416 | 537 | TTCCCAAAAGT TCCAAAGTAGACA A[C/G]AGTAATC GCCGTACTG CAGCAGG | C | G | Asn (1294) | Lys (1294) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. | 3.20E-127 |
| 922 | cg29351416 | 574 | GTTACTGCAGC AGGTCTCATTAC CA[G/T]ACATTG CTGGAACTATA CCGTCAAG | G | T | Asp (1295) | Tyr (1295) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. | 3.20E-127 |
| 923 | cg4398372 | 481 | TTGTTCCTCACT TAATTTATTTT [C/T]CTGCTTGGT CTTCTTCTTCA TCCT | C | T | Gly (1296) | Glu (1296) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBLNEW-ACC:AAD40376 PTD013 - HOMO SAPIENS (HUMAN), 243 aa. | 1.50E-123 |

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| 924 | cg44930828 | 658 | CCTCAAGGTTTC GCTGCCGAAGC TT[G/A]CCAACG TGCAGCTCCCTG GATACCGA | G A | Ala Thr (1297) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 925 | cg44930828 | 680 | CTTGCCAACGTC GCAGGCTCCCTGG ATA[CG]TCGACG GGGGTTTTGTG CACTCGGAC | C T | Thr Ile (1298) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 |
| 926 | cg44035718 | 919 | CTGGAGTAGCCA GGAGAACTGAG GGT[C/T]CCACT ACAAGGACATG CTCAGCGAA | C T | Ser Phe (1299) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA83010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment). | 2.20E-121 |
| 927 | cg44921277 | 571 | TTGGGGCAACCTT CCCCATCACCTT C[G/A]CCTGCTA TGCGGCCCTCT TCTGGCT | G A | Ala Thr (1300) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q35682 MYELOID UPREGULATED PROTEIN - Mus musculus (Mouse), 296 aa. | 1.70E-120 |
| 928 | cg43250166 | 461 | GCCGTTGATTTC CTCAGTGCCA TCTCCTGTGCA GATGCTCATCTC GGCTCTCG | C T | Glu Lys (1301) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa. | 3.30E-102 |

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| 929 | cg39512856 | 344 | CTTTTCCAGGC TTCCAGCAACG AG[G/A]TTCTC CTTCGGTGCAT TTCCAG | G | A | Thr (130) | Ile (1302) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 |
| 930 | cg39512856 | 517 | GCGGTCCACTT CTGATATCCCC [TC]CCGGGA TAACCAGGTAA ATTTC | C | T | Gly (1303) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 931 | cg39512856 | 536 | TCCCTCCGG CGATAACCAGG TAA[A/C]ATTTC CGGTAACGGAC CGAGTTCA | A | C | Phe (1304) | Val (1304) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 |
| 932 | cg39512856 | 638 | TGGTCTTCAACG AGATGCCACGA TG[C/A]CTCATC ACTGTTGAAAAC AGCCACA | C | A | Ala (1305) | Ser (1305) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 |
| 933 | cg39570960 | 851 | GCCTCCAGGA GTCGTTGTGTT TG[A/G]GCTGAA CGAATGTGCCGT CCAGCCGC | A | G | Glu (1306) | Gly (1306) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTRMBL- ACC:O14997 3-7 GENE PRODUCT- HOMO SAPIENS (HUMAN), 709 aa (fragment). | 2.60E-93 |
| 934 | cg43980391 | 510 | AGTAAATGGACA AGAATATCATCT [TC]AACTTGT GACACAGGGGG GCAAGA | C | T | Gln (1307) | End (1307) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTRMBL- ACC:Q15382 RAS-RELATED GTP- BINDING PROTEIN - HOMO SAPIENS (HUMAN), 184 aa. | 2.10E-90 |
| 935 | cg43983527 | 991 | TTCGGAAAGGAT GGTGACCCCTG GT[G/T]CGGCCG CCATTACTGGCA GAGTCCTG | G | T | Cys (1308) | Phe (1308) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa. | 6.50E-90 |
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| 936 | cg42341305 | 114 | GATGAATTCG AGTACAGACAC AC[C/T]GTATCC CGCAGGCCAAC CTCCAGAA | C T Pro (1309) | Leu (1310) His Gln T Gln C T C A | NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE | SIFIED SIFIED SIFIED SIFIED SIFIED SIFIED SIFIED SIFIED SIFIED SIFIED SIFIED SIFIED | UNCLAS Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa. | 8.10E-90 |
| 937 | cg43980889 | 737 | CTTCTATTGA ATTCTAAAGACC AT[G/T]TACAAGT AGAAAATGATGC TTAC | T G G G C T Gln End (1311) | Gln (1310) His Gln T Gln TAAAGACCATT A[CT]AAGTAGA AAATGATGCTTA CCCTGG | NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE | UNCLAS Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 938 | cg43980889 | 741 | TATTGAAATT TAAAGACCATT A[CT]AAGTAGA AAATGATGCTTA CCCTGG | C T Gln Glu C Glu | End (1311) Gln TAAAGACCATT A[CT]AAGTAGA AAATGATGCTTA CCCTGG | NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE | UNCLAS Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 939 | cg43980889 | 781 | TACCGATAAAC AG[AC]AAATGTT AAATATAGACAA GTGGAC | A C G T T Ala Ser (1312) | TACCGATAAAC AG[AC]AAATGTT AAATATAGACAA GTGGAC | NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE | UNCLAS Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 940 | cg29349483 | 146 | GCAGTTTCAC CAAGATCAAGA CC[G/T]CTGACCC ACCAAGTACATG GAGGGCTT | G T Ala Ser (1313) | GCAGTTTCAC CAAGATCAAGA CC[G/T]CTGACCC ACCAAGTACATG GAGGGCTT | NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE | UNCLAS Human Gene Similar to SPTREMBL- ACC:Q61081 CDC37 HOMOLOG - MUS MUSCULUS (MOUSE), 379 aa. | 2.00E-88 | |
| 941 | cg43918287 | 641 | TCTATGGCATCA TCCTGCATGAC CA[C/T]TGTGC ATCTAAACCA CCAGCCCC | C T Val Met (1314) | TCTATGGCATCA TCCTGCATGAC CA[C/T]TGTGC ATCTAAACCA CCAGCCCC | NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE | UNCLAS Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment). | 7.30E-84 | |
| 942 | cg43918287 | 651 | CATCTGCTGATGA CCACTTGTGCAT CIT/GAAACCAG CCCAGCCGCA ACCCCCA | T G Leu Phe (1315) | CATCTGCTGATGA CCACTTGTGCAT CIT/GAAACCAG CCCAGCCGCA ACCCCCA | NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE NON- CONSERVATI VE | UNCLAS Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment). | 7.30E-84 | |

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| 943 | cg43918287 | 676 | TAAACCAGCCC AGCCGCCAAC CCCA(G)AAAGT TGGCTGCAGTT ATTTAAT | A | G | Leu (1316) | Ser (1316) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment). | 7.30E-84 |
| 944 | cg43918287 | 693 | CAACCCCCAAA AGTTGGTCTGC AGTT(C)ATATTA ATTGAGGTTGG ACCTGGG | T | C | Ile (1317) | Met (1317) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment). | 7.30E-84 |
| 945 | cg37027086 | 217 | GAATCAGAACTA CAAGGATCAATT A[T]C]CCAGCT CAATGTCAGGG TTCTTCA | T | C | Ser (1318) | Pro (1318) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA76824 KIAA0980 PROTEIN - HOMO SAPIENS (HUMAN), 1406 aa (fragment). | 1.20E-83 |
| 946 | cg426888841 | 430 | ATTATAACTGGG ATCCCAGTCAAC A[T]AAGGTAG AATTTCATTAAC CTCAAG | T | A | Met (1319) | Leu (1319) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 |
| 947 | cg426888841 | 598 | CGGAGCCTAGT GCCAGGGCGGC GGC(A)AGACA GAGCTGTCAGA GGGGGACCC | A | C | Cys (1320) | Gly (1320) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 |
| 948 | cg40332814 | 339 | ACTGCACAGGG ACCGAATCTCTG CCIT/C]CCCGCT CTGCAGGCCAGG TGCTCCAA | T | C | Glu (1321) | Gly (1321) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA74864 KIAA0841 PROTEIN - HOMO SAPIENS (HUMAN), 641 aa (fragment). | 3.10E-83 |
| 949 | cg43920571 | 2059 | GGGTTTTCTCT CACGTCGGTCT GA[G(A)ATTACT GAGGAATTGTT GCTGGC | G | A | Ser (1322) | Phe (1322) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P34624 HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III - Caenorhabditis elegans, 548 aa. | 3.50E-82 |

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| 950 | cg44024149 | 451 | GGAAGCCGCAC | T | C | Tyr | His (1323) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa. | 5.30E-79 | 1 (1p35) |
| 951 | cg43307245 | 156 | GATATGATACTA | A | G | Glu | Gly (1324) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15488 GLYCOGENIN-2 ALPHA - HOMO SAPIENS (HUMAN), 501 aa. | 1.00E-75 | X |
| 952 | cg39523553 | 698 | GTGTGAGGTCT | G | A | Gly | Ser (1325) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC: CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |
| 953 | cg39523553 | 861 | ATGGCTCTTTCT | T | C | Leu | Pro (1326) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC: CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |
| 954 | cg35933325 | 312 | ACCAAATGCCA | A | C | Asn | Lys (1327) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC: BAA74845 KIAA0822 PROTEIN - HOMO SAPIENS (HUMAN), 1581 aa. | 2.40E-74 | |
| 955 | cg41677120 | 325 | CACGACCCACG | A | G | Lys | Glu (1328) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 1.10E-71 | 11 |

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| 956 | cg41677120 | 330 | CCCACGAGATC ATGGGCCCAA GAA[A/C]AAGCA CCTGGACTACTT AATTCACT | A C | Lys (1329) | Asn (1329) NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 1.10E-71 11 |
| 957 | cg41677120 | 382 | CACAAATGAGATC GAATGTGAACAT C[C/T]CACAGTT GGAGACAGTT TATTGA | T Pro | Ser (1330) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 1.10E-71 11 |
| 958 | cg39648832 | 208 | TGCAGCCTCGT CCTCCCTCCCTCTG GC[A/T]GGCTCT GCACACTCTGC TCCTGGTA | A T | Leu (1331) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA76807 KIAA0963 PROTEIN - HOMO SAPIENS (HUMAN), 1366 aa. | 3.20E-70 |
| 959 | cg42696021 | 412 | GACACCCGGCAC CGGGGCATGCT TC[A/G]ACAGT GGCTGTGCCGC CTTCACAAAT | C G | Thr (1332) | Arg (1332) NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa. | 1.40E-69 |
| 960 | cg42696021 | 421 | ACCCGGGCATG CTTCACACAGTG GC[T/C]GTGCCG CCTTCACAATGA AGTGAAC | T C | Leu (1333) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa. | 1.40E-69 |
| 961 | cg34243633 | 269 | CAGAGATAATG CAGGCCAGGGA GGA[G/C]ATTGC ACTGGATGTCA CCATCATGG | G C | Ile (1334) | Met (1334) NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. | 1.30E-68 |

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| 962 | cg34243633 | 453 | ACCGACATAAG AACTTGTTC AG[CT]GGGA GCAGCATGGCA ACCAGTGT | C T Ser (1335) | Asn (1336) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. |
| 963 | cg43942922 | 308 | CCTGAGCTCCA GCCCTCCACCT CCAC[G]AGACC AGCCTGTCACC TCTGAGGCC | C G Thr (1336) | Arg (1336) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. |
| 964 | cg43942922 | 317 | CAGGCTTCCAC CTCCACAGACC AGC[C/T]TGTC CCTCTGAGCCC ACATCTCAG | C T Pro (1337) | Leu (1337) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. |
| 965 | cg43942922 | 325 | CACCTCCACAG ACCAAGCCTGTC ACC[T/C]CTGAG CCCACATCTCA GGCCACTAG | T C Ser (1338) | Phe (1338) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. |
| 966 | cg43942922 | 341 | CCTGTCACCTCT GAGCCCCACATC TC[A/G]GGCCAC TAGGGGAAGAA AAAATAGG | A G Gln (1339) | Arg (1339) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. |
| 967 | cg35133436 | 291 | TTCTCTAGTCCA CCAGGAGGCTA CA[A/G]CTCGGC TCTCAGGGTCA GGTAATGA | A G G (1340) | Thr Ala (1340) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60369 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa. |

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| 968 | cg44938009 | 1289 | GAGTGCACGCA TAAGATGGAA GAG[G/T]ATGCA CTACTTCTGAT CCAGTGGAA | G | T | Asp (1341) | Tyr (1341) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO- TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 58 aa. | 5.80E-66 | X |
| 969 | cg43949821 | 287 | ATTTAATTCCCT TCCTGTCTACCG GC[G/A]GTTGGAA CCTCCTGGCTC TCTGCTGT | G | A | Arg (1342) | Cys (1342) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34394 NUCLEAR PORE COMPLEX INTERACTING PROTEIN NPIP - HOMO SAPIENS (HUMAN), 350 aa. ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 3.80E-62 | |
| 970 | cg39576123 | 681 | TGGCTTGGCT GGGGGCCATC AAT[C/T]CCAGC ATGGCTGCC CAGCAGTCC | C | T | Pro (1343) | Ser (1343) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.10E-62 | |
| 971 | cg42731307 | 347 | CGAAAAGCAA GTGCAGTTGTT GC[T/C]TCGGCT GTGAGTGGT CGGGTCCA | T | C | Ser (1344) | Gly (1344) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |
| 972 | cg42731307 | 488 | TCTGGAAAAGAA GGCATTGATGAT CC[G/A]GTCCCC CAGTGGGTTGA TGGCAAGT | G | A | Arg (1345) | Trp (1345) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |
| 973 | cg42731307 | 524 | GGTTGATGGCT AAGTTCTGGAT CC[T/C]CTGGAA ATCTCCGGCT GAGAGTC | T | C | Arg (1346) | Gly (1346) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |
| 974 | cg44910937 | 648 | TGCCCTGGAAC AGGAATATGAAA A[G/T]AAACTCA GAGCCGAGTTA GTGAAA | G | T | Lys (1347) | Asn (1347) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20716 F53B7.3 - CAENORHABDITIS ELEGANS, 267 aa. | 2.60E-61 | 3 |

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| 975 | cg43335624 | 149 | TCGAAAGGAAG TGAGTGCAGAT GG[G/A/G]AGACC ATCACTGTCACT TTCTTTAA | A | G | Lys (1348) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62184 T-COMPLEX PROTEIN 10C (TCP-10) - MUS MUSCULUS (MOUSE), 438 aa. | 7.00E-61 |
| 976 | cg43277268 | 448 | CGCTTAATGCCA AGAAGGGAGATG GTG[C/A]GCTCC AAGCTGCCAA CAGTGTGCT | C | A | Arg (1349) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62184 T-COMPLEX PROTEIN 10C (TCP-10) - MUS MUSCULUS (MOUSE), EHD1 - MUS MUSCULUS (MOUSE), 534 aa. | 3.90E-60 |
| 977 | cg44128084 | 724 | CTTGACATCCAGA CCAGACGGTTC AG[A/G]ATCAGC GGTTCTGTGGT GCGACCGGG | A | G | Glu (1350) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCOLOSIS, 307 aa. | 1.70E-59 |
| 978 | cg30455661 | 322 | TCTCAAGTGGT TTGAAGTCAAAC A[G/T]ATTTCAAC AGAAGAAATCA GCCCTC | G | T | Gln (1351) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa. | 5.20E-58 |
| 979 | cg42747615 | 31 | TGTGATAAAAGT CACTTTCAAGGC CAT[C/T]CACAG CGAATCTTCAGA CACTTT | T | C | Ile (1352) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14693 HYPOTHETICAL PROTEIN KIAA0188 - Homo sapiens (Human), 899 aa (fragment). | 1.60E-57 |
| 980 | cg43153425 | 276 | AAAATTACTAT GGTTCTACTG AA[T/G]CTCGGG TTGACTACATGG GCTCAAG | T | G | Ser (1353) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 |
| 981 | cg43968980 | 1093 | TATTTCTGCTT CTCTAACAGCTG AC/A[T/G]TAATT GCTTCCCTTGAAG CTGAAG | C | A | Ser (1354) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.50E-56 |

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| 982 | cg30384142 | 173 | GATA GTGGTGT GTGGTGA TGC AGT[A/T]AACCT GAC GAATGGTT AGCTGAAT | A | T | Lys (1355) | End (1355) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P44788 SUN PROTEIN (FMU PROTEIN) - Haemophilus influenzae, 451 aa. | 5.30E-56 | |
| 983 | cg43957773 | 445 | GGGCTCACCGT AGAGCAACTGC AAT[C/A]GCTCT GGGCCTGGGCC TGACAGGA | C | A | Asp (1356) | Tyr (1356) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43914 DNAX ACTIVATION PROTEIN 12 - HOMO SAPIENS (HUMAN), 113 aa. | 3.30E-54 | 19 |
| 984 | cg43931038 | 464 | AGGGCAACTTG TGGGCAACCTG GTC[I/A/C]AGGAA ACCTTGACTTCT TCAAATTG | A | C | Leu (1357) | Trp (1357) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 985 | cg43931038 | 588 | CCTCCCCCAT GCGATGCCAA CACT[C]TTGC GAGTGATGGCC TTGAAAGGG | T | C | Ser (1358) | Gly (1358) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 986 | cg43971060 | 686 | CCCACCTCGTT CGTGCTCCCCAC CCT[C/T]CCCAAG CTCCACCGCCT GGTCTTCAG | C | T | Pro (1359) | Ser (1359) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P31639 SODIUM/GLUCOSE COTRANSPORTER 2 (NA(+))/GLUCOSE COTRANSPORTER 2 (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 672 aa. | 4.20E-53 | |
| 987 | cg44010070 | 541 | TTCTCTGCCGG CACCTACCCGC GCC[T/G]GGAGG AGTACCGCCGG GGCATCTTA | T | G | Leu (1360) | Arg (1360) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O35775 SYNCOLLIN (SIP9) - Rattus norvegicus (Rat), 145 aa. | 6.40E-51 | |

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| 988 | cg43298242 | 145 | TCTGGGCAG GGCTCACAGAG ACG[G]GGTG AGGGAGAGAT CGTGGTTC | G A | Pro (1361) | Leu (1361) | NON- CONSERVATI VE | water_ch annel | Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 1.30E-163 | |
| 989 | cg43298242 | 163 | AGAGACGGGG TGAGGGAGAG ATC[G/A]TGGGT TCATGAGATCCC ATCTGGG | G A | Thr (1362) | Met (1362) | NON- CONSERVATI VE | water_ch annel | Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 1.30E-163 | |
| 990 | cg43300636 | 440 | CCACAGCCGCC ACGCCAACCTC CCG[G/gap]CCC AGGCCAGGCC TATGCGCATCA | G gap | Gly (1363) | FAMESHIFT | ATPase_ associat ed | Human Gene SPTRMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) (AND CF(1))) - BOS TAURUS (BOVINE), 838 aa. | 1.70E-175 | | |
| 991 | cg43300636 | 446 | CGGCCACGCC ACCTCCGGCC CAG[G/gap]CCA GGCCTATGCC ATCACCATTG | G gap | Gly (1364) | FAMESHIFT | ATPase_ associat ed | Human Gene SPTRMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) (AND CF(1))) - BOS TAURUS (BOVINE), 838 aa. | 1.70E-175 | | |
| 992 | cg43250373 | 193 | CTGTGGGGTTG ACCCAGAACAA AGC[A/gap]TTGC CAGAAAACGTTA AGTATGGGA | A | gap | Leu (1365) | Cys (1365) | FAMESHIFT | ATPase_ associat ed | Human Gene Similar to TREMBLNEW-ID:G2921585 ECTO- ATPASE - MUS MUSCULUS (MOUSE), 495 aa. | 1.40E-100 (10q24) |

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| 993 | cg43132502 | 360 | GGCCCCAGTGC C AGTGGGTGGCA CCG[C/gap]CGA GGCTGCTGTTA CGGCTCATCTT | gap | Pro (1366) | Arg (1366) | FRAMESHIFT | ATPase - associated | Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa. | 9.40E-58 | 11 |
| 994 | cg42528468 | 284 | GCTCCTGCCCTG G GGAACAACCGG AAG[G/gap]TGA TGAAC TGAGCA ATGTGCAAAGA | gap | Val (1367) | Cys (1367) | FRAMESHIFT | cadherin | Human Gene Similar to SWISSPROT- ID:P05362 INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR (ICAM-1) (MAJOR GROUP RHINOVIRUS RECEPTOR) (CD54) - HOMO SAPIENS (HUMAN), 532 aa. | 8.40E-78 | 19 (19p13.3) |
| 995 | cg43264626 | 1150 | TTTGCCAGTTT C CTTCCTTGAGTTG G[C/gap]CCTCCA GGGCACCCACA GAGCTAAA | gap | Gly (1368) | Ala (1368) | FRAMESHIFT | cathepsi n | Human Gene SWISSPROT- ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa. | 4.10E-183 | 1 |
| 996 | cg43132668 | 1893 | CGATGGGTGCC G AGGGTGATTCC GGAG[G/gap]GCC CGCTGGTGTGT GAGGACCAAGC | gap | Gly (1369) | Ala (1369) | FRAMESHIFT | cathepsi n | Human Gene Similar to SWISSPROT- ID:P98119 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1 PRECURSOR (EC 3.4.21.68) (DSPA ALPHA-1) - DESMODUS ROTUNDUS (VAMPIRE BAT), 477 aa. | 3.90E-74 | 5 (5q33) |
| 997 | cg43132668 | 1894 | GATGCGTGCCA G GGGTGATTCCG GAG[G/gap]CCC GCTGGTGTGTG AGGACCAAGCT | gap | Gly (1370) | Ala (1370) | FRAMESHIFT | cathepsi n | Human Gene Similar to SWISSPROT- ID:P98119 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1 PRECURSOR (EC 3.4.21.68) (DSPA ALPHA-1) - DESMODUS ROTUNDUS (VAMPIRE BAT), 477 aa. | 3.90E-74 | 5 (5q33) |
| 998 | cg44924334 | 198 | AAAGCTAATTGA A GACTTATTCTC C[A/gap]AAAACT ACCAAGACTATG AGTATCT | gap | Lys (1371) | Lys (1371) | FRAMESHIFT | glycoprotein | Human Gene Similar to SWISSPROT- ID:Q13491 NEURONAL MEMBRANE GLYCOPROTEIN M6-B - HOMO SAPIENS (HUMAN), 283 aa (fragment), | 5.60E-76 | |

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| 999 | cg43303165 | 2549 | GGCCCCACTA TCAGGGCCCT GGC[C/gap]TCAA TCACTGAGACC ATCCAAGTCC | C | gap | Ser (1372) | FRAMESHIFT | histone | Human Gene Similar to SWISSPROT- ID:P53973 HISTONE DEACETYLASE HDA1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 706 aa. | 4.10E-70 | X |
| 1000 | cg42489148 | 881 | TGGAGTGGAT GGGAACCGGC GCA[G/gap]CAGT CCCTGGCAGC CAAGTAAAAA | G | gap | Ser (1373) | FRAMESHIFT | homeobox | Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL- TYPE HOMEBOX PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa. | 6.00E-118 | 13 |
| 1001 | cg43929210 | 483 | TCTGGCTCAGC ATGATGTTCCCT CT[G/gap]GCCTT CAGCCTGCCAC TAAGAAATG | G | gap | Ala (1374) | FRAMESHIFT | hydroxysteroid | Human Gene SWISSPROT- ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17-BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa. | 0.00E+00 | 5 |
| 1002 | cg44004587 | 1811 | GCTTATTTCGG TGTTGAATAAGA A[G/gap]ACACTA AAAGCTCGATG CAATAATC | G | gap | Val (1375) | FRAMESHIFT | isomers | Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa. | 3.00E-123 | |
| 1003 | cg41501665 | 156 | CGCTTCTCAA GGTGTGGAGG AGG[C/gap]GGC GGCCGCCGAGG AGGCCCTGCC | C | gap | Ala (1376) | FRAMESHIFT | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 | |
| 1004 | cg41501665 | 184 | CGCCGCCGAG GAGGGCCTGCG CGA[G/gap]CTGC AGCCAGCCGG CGGCTCTGCC | G | gap | Leu (1377) | FRAMESHIFT | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 | |

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| 1005 | cg41501665 | 202 | TGCCGAGCTG CAGCGAGCCG GG[G/gap]CTCT GCCACGAGGAC GTGAGGCAC | G gap | Leu (1378) | Ser (1378) | FRAMESHIFT | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 |
| 1006 | cg41501665 | 232 | GCCACGAGGAC GTGGAGGGCT GGC[C/gap]GCC ATCTACGGAGA GAAGGAGGCT | C gap | Aia | Pro (1379) | FRAMESHIFT | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 |
| 1007 | cg43939695 | 342 | CAAGACTGAGA TCAATTGCCGG CGGC[C/gap]CGG ACGATGGAAC CTCTTCCCCCT | C gap | Pro | Arg (1380) | FRAMESHIFT | kinasere ceptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 |
| 1008 | cg29023997 | 199 | TCTGGATGGGA TGAGCACCAT GTG[C/gap]GCAC CTGCATCCCCA AAGTGGAGCT | C gap | Arg | Ala (1381) | FRAMESHIFT | kinasere ceptor | Human Gene SWISSPROT- ID:P36896 SERINE/THREONINE- PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37) (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB) - HOMO SAPIENS (HUMAN), 505 aa. | 9.30E-280 |
| 1009 | cg43983535 | 4377 | CTCCAAACAGCT TCCTTCACTTTT T[G/gap]AGAAGG GCCTCTGCAGC TACCAACT | C gap | Leu (1382) | Leu (1382) | FRAMESHIFT | laminin | Human Gene SWISSPROT- ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSEN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa. | 0.00E+00 |
| 1010 | cg42488873 | 480 | TTCCCCTTAAT TGGTCAGCATA GT[G/gap]CCCCA TTTGGGGCATC CTTCAGCT | G gap | His (1383) | Thr (1383) | FRAMESHIFT | lipase | Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPOASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa. | 9.80E-261 |

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| 1011 | cg42488873 | 494 | GTCAGCATAGT GCCCCATTGG GGG[C/gap]ATCC TTCA[GCTGGAC AAGGGAAACA | C gap | Cys (1384) | Ser (1384) | FRAMESHIFT | lipase | Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa. | 9.80E-261 |
| 1012 | cg42488873 | 923 | CACGGGGCCC CCAGGCCTCCTG CCCC[G/gap]CCCT CGCGGCCGTG GCGGCCAG | G gap | Ala | Gly (1385) | FRAMESHIFT | lipase | Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa. | 9.80E-261 |
| 1013 | cg43249083 | 2329 | GGAGCAGCTCC AGGAGACGGCTG CTGIC/gap]GGG CTCTTCGGCT CTGGTGCTGAA | C gap | Arg | Gly (1386) | FRAMESHIFT | nucl_rec pt | Human Gene SWISSPROT- ID:P20393 V-ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa. | 0.00E+00 (17q11.2) |
| 1014 | cg43991048 | 6644 | TCTTTCTTTCTT CTTCTTTTTT C/gap]GTTTTT CTGCTTTATCCT CTTCT | C gap | Glu | Lys (1387) | FRAMESHIFT | nucl_rec pt | Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa. | 0.00E+00 17 |
| 1015 | cg43919677 | 4055 | GAAGAAAAAGAA AGAAATGCTACTA TA[Agap]TCTCA ATGACGCCAGT CTCTGTGAT | A gap | Asn | Ile (1388) | FRAMESHIFT | oncogen e | Human Gene SWISSPROT- ID:Q00918 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1- BP- 1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)- RATTUS NORVEGICUS (RAT), 1712 aa | 0 2 (2p12) |

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| 1016 | cg43997978 | 3546 | CATCAGCTCACT GTAGATTACCTC T[G/gap]CTTCGCT CAATGAGGGAT TCCACGGA | G | gap | Ala (1389) | Glu | FRAMESHIFT e | oncogen | Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa. | 2.9E-244 | 1 |
| 1017 | cg43916615 | 75 | ATGACGGAATATT AAGCTGGTGGT GGT[G/gap]GGCG GCCGGGGTGT GGCAAGAGT | T | gap | Vai (1390) | Gly | FRAMESHIFT e | oncogen | Human Gene Similar to TREMBLNEW-ID:G332185 TRANSFORMING PROTEIN (P21 HAS) - HARVEY MURINE SARCOMA VIRUS, 241 aa. | 3.1E-98 | |
| 1018 | cg43916615 | 76 | TGACGGAATATA AGCTGGTGGTG GT[G/gap]GGCG CCGGCGGTGT GGCAAGAGT | G | gap | Gly (1391) | Ala (1391) | FRAMESHIFT e | oncogen | Human Gene Similar to TREMBLNEW-ID:G332185 TRANSFORMING PROTEIN (P21 HAS) - HARVEY MURINE SARCOMA VIRUS, 241 aa. | 3.1E-98 | |
| 1019 | cg43916615 | 77 | GACGGAAATATA GCTGGTGGTG TG[G/gap]GC CGGGGGTGTG GCAAGAGT | G | gap | Gly (1392) | Ala (1392) | FRAMESHIFT e | oncogen | Human Gene Similar to TREMBLNEW-ID:G332185 TRANSFORMING PROTEIN (P21 HAS) - HARVEY MURINE SARCOMA VIRUS, 241 aa. | 3.1E-98 | |
| 1020 | cg43069905 | 900 | AGCTCCAGCAG TGACAGGTCA CT[G/gap]CCCC CGTCGGCGTCA TACCGCATG | C | gap | Glu (1393) | Arg (1393) | FRAMESHIFT e | protease | Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP)- GALLUS GALLUS (CHICKEN), 475 aa. | 1.3E-57 | 13 |
| 1021 | cg43069905 | 904 | CAGCAGTGACA GGTCATTCTCCC CC[G/gap]CGCGTC CGCGTCATACC GCATGTGCA | gap C | Ala (1394) | Ala (1394) | FRAMESHIFT e | protease | Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP)- GALLUS GALLUS (CHICKEN), 475 aa. | 1.3E-57 | 13 | |

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| 1022 | cg44028327 | 904 | A ATATTCACTAC G[A/gap]ATTGCT TCCCTCTCACAG AACTGTG | A gap | Ile (1395) | Leu (1395) | FRAMESHIFT | protease1 nhib | Human Gene SWISSPROT- ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) - HOMO SAPIENS (HUMAN), 644 aa. | 0 3 (3q27) |
| 1023 | cg43940280 | 720 | CCTCGAAGTCT GCCTGGCACA CAC[C/gap]ACAT GCAGATTGGT GCTTCCCCA | C gap | Gly (1396) | Val (1396) | FRAMESHIFT | ribosoma iprot | Human Gene Similar to SWISSPROT- ID:P49207 60S RIBOSOMAL PROTEIN L34 - HOMO SAPIENS (HUMAN), 116 aa. | 7.6E-56 |
| 1024 | cg43974196 | 5050 | GATTCAGGCG TGTCCTGGGGT AAG[C/gap]CCAC AGGGTTGAGAA AGGAAACCTC | C gap | Pro (1397) | Pro (1397) | FRAMESHIFT | struct | Human Gene SWISSPROT- ID:Q02440 DILUTE MYOSIN HEAVY CHAIN, ISOFORM I (MYOSIN HEAVY CHAIN P190) (MYOSIN-V)- GALLUS GALLUS (CHICKEN), 1829 aa. | 0 13 (15q21) |
| 1025 | cg43916919 | 1130 | GAAGAAAGACGC CCTGGTTCTCTT GC[G/gap]CCACA GGCACCGGCTT CAGCTTCTC | G gap | Ala (1398) | Gly (1398) | FRAMESHIFT | struct | Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa. pols:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa. | 4.3E-188 2 (2cen) |
| 1026 | cg21428405 | 293 | ATCTCTTCAGGG GCCAGGGTCCGG GT[G/gap]GCCGA GGGGAAACGGGG TCGAGCTCG | C gap | Asp (1399) | Thr (1399) | FRAMESHIFT | synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.2E-56 |
| 1027 | cg43336100 | 290 | ATCATGCTGG GAACTCGCAGA TGA[G/gap]AGAG CGCATGCTGCT GCAAGCCACAG | G gap | Arg (1400) | Lys (1400) | FRAMESHIFT | tnf | Human Gene SWISSPROT- ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) - HOMO SAPIENS (HUMAN), 381 aa. | 2.2E-207 3 (3q25) |

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| 1028 | cg39517655 | 438 | GGGCCCTTAC TCGCTATGCTG CAAG/gap]GGC CCGGGCCTTG GCTCGGCCGC | G gap | Gly (1401) | FRAMESHIFT factor | transcript | Human Gene SWISSPROT- ID:Q14209 TRANSCRIPTION FACTOR E2F2 (E2F-2) - HOMO SAPIENS (HUMAN), 437 aa. |
| 1029 | cg43954704 | 1391 | CCCACTGGAAAG TGGAGGCTCCA GTCAA/gap]AAC CCCCTCTGAGC TCCGAGGCAG | A gap | Phe (1402) | FRAMESHIFT factor | transferring | Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC-POLYPEPTIDE ALFA-1,0 N-ACETYLGLACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa. |
| 1030 | cg43936426 | 1227 | GCGGACAGTGTG CCCTTAAGCAGT GCAA/gap]GGTG TCTTGAGCCCA TGGTGGCCA | A gap | Arg (1403) | FRAMESHIFT factor | ubiquitin | Human Gene SWISSPROT- ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa. |
| 1031 | cg4397221 | 2853 | GAAATGTCATCC ACGGTATTTTTT TT/gap]CAGTTT TAGTTTGACCAA AGCTTTA | T gap | Lys (1404) | FRAMESHIFT factor | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13563 POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTWIN) (R48321) - Homo sapiens (Human), 968 aa. |
| 1032 | cg43918356 | 2640 | ATGTCATCTCA TCTAGAAAACGCC CC[gap/A]TCACG GAAATGGAATTG CTGCCAGA | A gap | Arg (1405) | FRAMESHIFT factor | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN. HOMO SAPIENS (HUMAN), 783 aa (fragment). |
| 1033 | cg43918446 | 2812 | CTTCCCCACATG ACTTGTACATT C/C/gap]GACCAAC TGGGACCACTC GGTGAGCT | C gap | Ser (1406) | FRAMESHIFT factor | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa. |

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| 1034 | cg43927750 | 2857 | TAAAAGTTATT TCCAATGGTGT T[G/gap]GGCAAG CCCTGCCTCT GTATTCTT | G gap | Pro (1407) | FRAMESHIFT SIFIED | UNCLAS | Human Gene SWISSNEW- ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa. | 0 X (Xq28) |
| 1035 | cg43961075 | 1344 | GGTAGGATTG CTCATTTCAGGG CA[G/gap]CTGTC GCAAGCATCTC CCACCCCGT | G gap | Ser (1408) | FRAMESHIFT SIFIED | UNCLAS | Human Gene SWISSPROT- ACC:P49746 THROMBOSPONDIN 3 PRECURSOR - Homo sapiens (Human), 956 aa. | 0 1 |
| 1036 | cg43961763 | 1192 | CATCTAGGTCAA CAGGAAGGTC AG[G/gap]CTCCG CTCCGGTTCCA CTGATCCAT | C gap | Glu (1409) | FRAMESHIFT SIFIED | UNCLAS | Human Gene SWISSPROT- ACC:P13521 SECRETOGRAIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa. | 0 2 |
| 1037 | cg43968223 | 2979 | GTTCCTGTTCTTG TAGCGCTTTCTG C[G/gap]CTGCAG CATGATCTGAAG CTTGTG | G gap | Arg (1410) | FRAMESHIFT SIFIED | UNCLAS | Human Gene SPTREMBL- ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment). | 0 14 |
| 1038 | cg43980727 | 2673 | CCCTCCAGGTA GAGGCCCTAGGA AGGC[G/gap]CCCA GAACTGAAAGCC GAAGCGCTGG | C gap | Ala (1411) | FRAMESHIFT SIFIED | UNCLAS | Human Gene SWISSPROT- ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa. | 0 17 |
| 1039 | cg43999667 | 3941 | TTCTGTTTGTCT AGGACTTTTT T[G/gap]CTACA GTTGTTTCTG GGATCAC | T gap | Glu (1412) | FRAMESHIFT SIFIED | UNCLAS | Human Gene SPTREMBL- ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment). | 0 6 |
| 1040 | cg44022781 | 3927 | GTATCAAAGTGC TCTTCCAAACTT TT[G/gap]GGAGGC CCCATCACCCT ACCGGTA | T gap | Pro (1413) | FRAMESHIFT SIFIED | UNCLAS | Human Gene SPTREMBL- ACC:Q14692 KIAA0187 PROTEIN - HOMO SAPIENS (HUMAN), 1282 aa. | 0 |

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| 1041 | cg44919370 | 571 | CGTGGACTTTCCGAGGATGACCC[CGap]TGGAGGCCACTGTCCA TTGGCCCC | C gap | Leu | Trp (1414) | FRAMESHIFT UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60624 CLASS I CYTOKINE RECEPTOR - HOMO SAPIENS (HUMAN), 636 aa. | 0 | 19 |
| 1042 | cg44932924 | 2612 | TCTACAACCAGAGC GCCAGGAATTACAG[Gap]ACGAA GCTGGAGGACTGCAGGAACA | G gap | Thr | Arg (1415) | FRAMESHIFT UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92574 HAMARTIN (MYELOBLAST KIAA0243)- HOMO SAPIENS (HUMAN), 1164 aa. | 0 | 9 |
| 1043 | cg43991434 | 1167 | GGGGTGCAAGGGC GCCTGGGAAATA[G/gap]CCT GCTGCACCATG TGGTTTCAGCG | G gap | Asp | Asp (1416) | FRAMESHIFT UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa. | 1.7E-304 | 22 |
| 1044 | cg44931278 | 1264 | CCTCTCCAGGA GAAGGCACTGGC CAG[G/gap]CCT GCAGGTGTAGGC CACTTCTGCA | G gap | Asp | Asp (1417) | FRAMESHIFT UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa. | 4.5E-280 | 1 |
| 1045 | cg43949042 | 427 | CACAGCTGCGTTGCCATAGTTGC CC[G/gap]GGAAA AAGGGCCCCAAC GAACCAGGC | T gap | Gln | Arg (1418) | FRAMESHIFT UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa. | 6.10E-268 | |
| 1046 | cg43972066 | 2313 | TAAATTTGACTTA TTCTCATGTAAA A[A/gap]GTCTA ATGCAGATGTATT TGGTAAT | A gap | His | His (1419) | FRAMESHIFT UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60747 PUTATIVE G-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 562 aa (fragment). | 4.10E-221 | 10 |

| 1047 | cg43955639 | 723 | GGGGTACTGG GGACCTCGTCT GTT[G/gap]GGT CCCTCCCTCA GGTAGGGC | G gap | Pro (1420) | Gln (1420) | FRAMESHIFT UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment). | |
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| 1048 | cg43955639 | 725 | GGGTACTGGGG ACCTCGTCTGTT GG[G/gap]TTCCC CTCCCTCCAGGG TAGGGCTC | G gap | Asn (1421) | FRAMESHIFT UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment). | 2.80E-215 | |
| 1049 | cg43965656 | 391 | CTGCCTATTCTG AACCAAGCCAAC AT[C/gap]TGAGA TTTTGCCAATG CCCGAGGT | C gap | Ser (1422) | Leu (1422) | FRAMESHIFT UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q99541 ADIOPHILIN - HOMO SAPIENS (HUMAN), 437 aa (fragment). | 7.20E-210 |
| 1050 | cg43944615 | 2370 | TACATGGCAC GAGGAAGAAC GCA[G/gap]CAC GGCGCTGCAGT TCACGTCCACCC | G gap | Leu (1423) | Cys (1423) | FRAMESHIFT UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O14877 FRPHE - HOMO SAPIENS (HUMAN), 346 aa. | 1.30E-192 |
| 1051 | cg43323906 | 334 | CTCTGGTGTG CTCCCTCTGAAGA TT[G/gap]AAGCT TATTCAATGAG ACTGCAGA | C gap | Gln (1424) | Lys (1424) | FRAMESHIFT UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42081 T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2 ANTIGEN) (CTLA-4 COUNTER- RECEPTOR B7-2) (B70) (FUN-1) (BU63) - Homo sapiens (Human), 329 aa. | 1.80E-174 |
| 1052 | cg44004690 | 251 | GAGGAGGAGGA GGTGGAGGAGG AGG[A/gap]GGG AGAAGAGGATG TTTACCGAG | A gap | Glu (1425) | Gly (1425) | FRAMESHIFT UNCLAS SIFIED | Human Gene TREMBL NEW- ACC:BAA74892 KIAA0869 PROTEIN HOMO SAPIENS (HUMAN), 888 aa (fragment). | 2.50E-161 |

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| 1053 | cg44004690 | 402 | ACCGGAGAGTG GGCACCCCGTC CCAG/gap)GGG CCATTCTTCGA GGGAGCACCA | G gap | Gly (1426) | FRAMESHIFT SIFIED | UNCLAS | Human Gene TREMBLNEW- ACC:BAA74892 KIAA0869 PROTEIN - HOMO SAPIENS (HUMAN), 888 aa (fragment). | 2.50E-161 |
| 1054 | cg43957283 | 322 | TCGAGGGTGAC CACAGCCCCAG AGGG(gap)CCG CAGCACAGGCC AGGGGGTGGCG | G gap | Pro (1427) | FRAMESHIFT SIFIED | UNCLAS | Human Gene TREMBLNEW- ACC:AAD27734 CGI25 PROTEIN - HOMO SAPIENS (HUMAN), 301 aa. | 1.40E-160 |
| 1055 | cg43329741 | 336 | GCTCTACCTGG GCTACACCCCCG CAGIG/gap)CGG CCCGTGAAAGTG CGCATCATGCA | G gap | Ala (1428) | FRAMESHIFT SIFIED | UNCLAS | Human Gene TREMBLNEW- ACC:AAD39906 FH1/FH2 DOMAIN- CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa. | 6.70E-159 |
| 1056 | cg44010310 | 501 | TTTGGTTGAGATG CATGAAATTTTT Tgap/TCTCTATT GCTGCTTGAAAA TTTACA | gap T | Lys (1429) | FRAMESHIFT SIFIED | UNCLAS | Human Gene TREMBLNEW- ACC:BAA32101 BCAP - HOMO SAPIENS (HUMAN), 331 aa. | 1.30E-155 |
| 1057 | cg39729127 | 981 | GCTCTCTCTTT ATTGGTAACCGAG Tgap/TGGTGGC CACGAGTCATA CAGGGAAA | gap T | Val (1430) | FRAMESHIFT SIFIED | UNCLAS | Human Gene TREMBLNEW- ACC:AAD42876 NY-REN-45 ANTIGEN - HOMO SAPIENS (HUMAN), 815 aa. | 3.00E-152 |
| 1058 | cg43135797 | 861 | AGATCTGTCTCC CGGAGAACCCG GA[Gap]CCGCT GGCCATTGCAG AAGGGCCC | G gap | Leu (1431) | FRAMESHIFT SIFIED | UNCLAS | Human Gene Homologous to SWISSPROT-ACC:Q14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa. | 1.60E-150 |

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| 1059 | cg43965796 | 1704 | ATCACTGTTGAT GCTCTGGGCCA CG[C/gap]CAGG GTACTGGATCTT CATGGCCAC | C gap | Gly (1432) | FRAMESHIFT SIFTED | UNCLAS | Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment). | 9.00E-148 |
| 1060 | cg43965796 | 1705 | TCACTGTTGATG CTCTGGGCCAC GC[C/gap]AGGG TACTGGATCTC ATGGCCAC | C gap | Gly (1433) | FRAMESHIFT SIFTED | UNCLAS | Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment). | 9.00E-148 |
| 1061 | cg42907867 | 1100 | AGGGGCCACGGG GTGGGCCAGGG GGC[C/gap]GGG CCATTTCAGTG GCTCCCTTGTC | C gap | Arg (1434) | FRAMESHIFT SIFTED | UNCLAS | Human Gene Homologous to SPTREMBL-ACC:Q99769 HYPOTHETICAL 26.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 255 aa. | 1.10E-140 |
| 1062 | cg43922710 | 126 | TCTACCCAGCTA AATACACATTAT G[G/gap]CATTAA GCAAACTAACCT ACAAGTC | G gap | Ala (1435) | FRAMESHIFT SIFTED | UNCLAS | Human Gene Homologous to TREMBL NEW-ACC:BAA74897 KIAA0874 PROTEIN - HOMO SAPIENS (HUMAN), 601 aa (fragment). | 4.90E-140 |
| 1063 | cg43303845 | 1073 | GCAGGAACGCC TGGATCGGGAG AGG[C/gap]AAGA AAGACAAGAAC GAGGAGGCT | C gap | Gln (1436) | FRAMESHIFT SIFTED | UNCLAS | Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa. | 1.90E-138 |
| 1064 | cg43973762 | 430 | ATAACAGAAAGC AAGAGAAAGTGT GAI[G/gap]AACTC TGAAAGAAAGAA GTTAAAAAG | G gap | Arg (1437) | FRAMESHIFT SIFTED | UNCLAS | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.20E-137 |

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| 1065 | cg43918679 | 411 | TCA CAG ATAT CT CCATTGGCAG GA[gap]ATGCC CAGCCTGGAGG TGATCACGC | G gap | Met Ile | Cys (1438) (1439) | FRAMESHIFT SIFIED | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa. | 3.00E-131 4.00E-129 | 21 |
| 1066 | cg38059286 | 503 | GCG GCT CCC T TTCTCACTGAAG CA[gap]ATCT CCAGGAGACA AAGACCTGG | G gap | Ser Ser | FRAMESHIFT SIFIED | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD39906 FH1/FH2 DOMAIN-CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa. | 3.70E-126 | | |
| 1067 | cg42549778 | 1014 | ACT GTCACTTCC CTGCTGCAGGG CA[gap]CCCC ACCTGTGAGTG GCTCGAGCC | G gap | Ser Thr (1440) | FRAMESHIFT SIFIED | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa. | 1.70E-120 | | |
| 1068 | cg44921277 | 516 | CCC TGATCATCC TCATCGTGGAG CT[gap]GCGG GCTCCAGGCC GCTTCCCCC | G gap | Cys Ala (1441) | FRAMESHIFT SIFIED | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O35682 MYELOID UPREGULATED PROTEIN - Mus musculus (Mouse), 296 aa. | 1.70E-120 | | |
| 1069 | cg44921277 | 518 | CTGATCATCCTC ATCGTGGAGCT GT[gap]CGGG CTCCAGGCC CTTCCCCCTG | G gap | Cys Ser (1442) | FRAMESHIFT SIFIED | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O35682 MYELOID UPREGULATED PROTEIN - Mus musculus (Mouse), 296 aa. | 1.70E-120 | | |
| 1070 | cg42530218 | 327 | GATTTAAATACAC AGCAGCAGCAG CA[gap]GAACTA CATTAGGTGCT CTCTTCAGT | gap G | Gln Gln (1443) | FRAMESHIFT SIFIED | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa. | 2.00E-118 | | |

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| 1071 | cg42530218 | 329 | ATTTAATAACACA GCAGCAGCAGC AA[Agap]CTACA TTAGGTGGTCTC TTCA GTCA | A gap | Thr (1444) | Leu (1444) | FRAMESHIFT SIFIED | UNCLAS SIFIED |
| 1072 | cg43325007 | 979 | AGGATAACCCCC GAGGAAGGCCG CCA[G/gap]GAAT GCGTGTGCTGG GTAGGTCTTG | G gap | Leu | Trp (1445) | FRAMESHIFT SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa. |
| 1073 | cg43981269 | 776 | GGCCTACGGCG CCTACGGCTCAG GCA[C/gap]TGAT GCAGCAGCAA CGGCCCTGAT | C gap | Leu | End (1446) | FRAMESHIFT SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa. |
| 1074 | cg43250166 | 166 | AGGTGGCCCTC ACACCCAGTGC TGT[G/gap]CTGC GCGGAGGGCTG TACTGAAGGT | G gap | Ala | Asp (1447) | FRAMESHIFT SIFIED | Human Gene Homologous to SPTRMLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa. |
| 1075 | cg43982164 | 778 | CTGGGGGGGT GCTCATCCTGG ACA[Agap]CATT ACCTGCCTCC TGTCTTCCA | gap | C | Asn | Thr (1448) | FRAMESHIFT SIFIED |
| 1076 | cg43980889 | 812 | TTAAATATAGAC AAGTGGACATT TT[G/gap]GCCTCA AATTACACAGGA GCCAGGCAT | T gap | Ala | Pro (1449) | FRAMESHIFT SIFIED | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHEICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. |
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| 1077 | cg43970119 | 832 | GTGCCATTGG TGAGACATCCAT | A | gap | Ile | Met (1450) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88719 CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLYLTRANSFERASE) (CMP- SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa. | 1.00E-82 | 12 |
| 1078 | cg44030987 | 447 | TGGCATGTTG AGTGGAACAGT TGT[Agap]TTTA CTTGAAATTCCAA TCTCTTCT | A | gap | Tyr (1451) | Thr (1451) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA76495 TYPE II MEMBRANE PROTEIN SIMILAR TO CD69 - HOMO SAPIENS (HUMAN), 149 aa. | 1.90E-81 | |
| 1079 | cg43320682 | 665 | GGGGCTCAGG GGCTGGGGAG GCT[Agap]CCCT GGGCCTTCAGA CAGCACATAG | C | gap | Glu (1452) | Ser (1452) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment). | 6.60E-81 | |
| 1080 | cg25255686 | 366 | AAGGCCACATC AAGTGGGGGT GGC[Agap]TTCG GGCATCTCCCT GCCGAGGGTA | C | gap | Phe (1453) | Ser (1453) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB39700 CONSERVED HYPOTHETICAL PROTEIN - STREPTOMYCES COELICOLOR, 384 aa. | 2.10E-77 | |
| 1081 | cg43988975 | 371 | CTCCCTCCTGAC CGAGTGGGGCCG GCA[Agap]GAG CTTGAATCGTC ATGGAGATG | G | gap | Glu (1454) | Ser (1454) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P50606 MAGO NASHI PROTEIN HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 146 aa. | 8.00E-76 | |
| 1082 | cg39523553 | 670 | CACTGGTATGC ACGGGGGGTC TCC[Agap]CAGT GTGAGGTCTGC CCGATCGGG | G | gap | Gln (1455) | Ser (1455) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |

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| 1083 | cg43951096 | 2953 | CTCCCTCCTGG GTATCTGCATCT TC[gap/A]AAAT CTCCTTCTTGGT TTTCATCC | gap | A | Glu | End (1456) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2.00E-71 | 17 |
| 1084 | cg42831353 | 806 | GGACACAGGGCT GCGGTGTAAGC CCG[C/gap]GTCA CCGCCGGCAC TGCAAGGAAC | C | gap | Thr | Thr (1457) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa. | 1.30E-67 | 22 |
| 1085 | cg44938009 | 688 | AATACTCCGTGC AGCGAGTGGGT CA[G/gap]CTCC TGAAAGAATTGA TCAAGGTC | G | gap | Leu | Ser (1458) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO- TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 587 aa. | 5.80E-66 | X |
| 1086 | cg43054992 | 315 | CAAATCACAGC TGAAAGAATGTA TG[gap]ATATA TTGGAAATATG GACCTAT | G | gap | Asp | Ile (1459) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34105 CGI- 110 PROTEIN - HOMO SAPIENS (HUMAN), 125 aa. | 4.60E-64 | 2 |
| 1087 | cg39516123 | 928 | CCTGGGGCTCA CCAAGGCAACC TGG[C/gap]CTCC GGTCTTCATAGC AATGCAATA | C | gap | Ala | Ala (1460) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.10E-62 | |
| 1088 | cg43983590 | 713 | GGAGGAGGCOAG GCGAGGCACACC CCC[C/gap]TGTT GGCCCCCTGCAC CGGCCAGCC | C | gap | Leu | Cys (1461) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q19498 SIMILAR TO MELIBIOSE CARRIER PROTEIN - CAENORHABDITIS ELEGANS, 501 aa. | 1.50E-60 | |

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| 1089 | cg44128084 | 499 | CGGGGGGCAT GCTGACGTTCTGC/C/gap/GTCT GTCGACGAGTT GCCGGTGCAA | C gap Arg | Ala (146) (1463) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.70E-59 |
| 1090 | cg44128084 | 524 | CGCTGTGAC GAGTTGCCGGT GCA[A/gap]CGCT GGAGCTGCGAC GGATCCCTGG | A gap | Ala (146) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.70E-59 |
| 1091 | cg43976473 | 931 | GGCCTGTGCT TGGAGCCGTGG GCT[C/gap]CGTA GCCGAGTGAT AAGCCATGGC | C gap | Gly (146) (1464) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa. | 3.50E-59 |
| 1092 | cg40309770 | 385 | TTCGGGGGCC GGCTCCAGGGC TCGC/C/gap]CCGC TGAGGTGTTTC ATGACCCCGC | C gap | Gly (146) (1465) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q60870 POLYPOSIUS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106) - Mus musculus (Mouse), 185 aa. | 4.10E-56 |
| 1093 | cg42725664 | 184 | AGATAGCTGAG AATATTCTGCC AA[G/gap]CCTCA CAGCTTGTTC TGGCAGGCC | G gap | Leu (1466) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA74896 KIAA0873 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa (fragment). | 1.5E-51 |
| 1094 | cg39380052 | 497 | ATGAGATCGAC GCCCTTGGCGGG CCG[C/gap]GGC GTAGACATTCC GCACCCGCTCA | C gap | Gly (1467) | FRAMESHIFT UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa. | 1.3E-50 |

CGTCAATCATG
CCGCTTAGAG
AA[T/gap]GCAAAC
ATGGGCAACCT
GATTGTGA

| 1095 | cg44928804 | 1181 | CTCTCAATCATG CCGCTTAGAG AA[T/gap]GCAAAC ATGGGCAACCT GATTGTGA | T gap | Cys (1468) | Ala (1468) | FRAMESHIFT SIFIED | UNCLAS | Human Gene SWISSPROT- ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO- NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa. | 9.1e-313 | 6 (6q14) |
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